STIC-Biotech/ChemLib

From: Sent:

Li, Ruixiang Thursday, July 11, 2002 11:37 AM STIC-Biotech/ChemLib

To:

Subject:

Sequence search of Application NO: 09/899,513

Please do a standard search on SEQ ID NOS: 1 and 2 against the commercial nucleic acid databases.

Thank you very much!

Ruixiang Li / GAU 1646 CM1 10E18 Mail Box 10C01 306-0282

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Searcher:
Phone:
Location:
Date Picked Up:フル
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:	
NA Sequences: 2	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

VENDOR/COST (where applic.) STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Run
              Result
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Maximum DB seq length: 2000000000
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                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
Query
Match Length
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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	04 2	34 2	35 1	97 2	46 1	16 2	55 2	77 2	60 2	96 1	86 2	45 1	42 5	20 9	46 2	73 2	62 9	60 2 A	26 1 9	07 2	14 1	62 1	07 2	80 2	28 9	25 6 P	95 9	95 6	34 9	05 2	20 9	40 2	80 2	80 6 A	44 6 2	20 6 7	4 9 09	25 6 A	19 9 A	19 9 н	19 6 A	19 6	16 6	15	47
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RESULT 1
AL354876/c
LOCUS
LOCUS
DEFINITION
PROCRESS ***, 3 unordered pieces.

ACCESSION
AL354876.9 GI:14575158
KEYWORDS
SOURCE
ORGANISM
ELWARYOCLE; HTGS_PHASEI; HTGS_DRAFT.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 152947)
AUTHORS
DIrect Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, Candenser; Clonerequestes and 201 this sequence version replaced gi:13234889.

COMMENT Center code: SC
Web site: http://www.sanger.ac.uk
Web site: http://www.sanger.ac.uk
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ALIGNMENTS

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BASE COUNT
ORIGIN
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                                                             ATGGGGGCTGCCTTTGTCGCTAGCCTCCGCAGTAACCTTTCTTCTGCCACTTCAAGGTCA 54026
ctcacctactacctgggcctggcccggaggccgcctgccacgcgggccggggccacctact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 152747; sum-of-contigs
Insert size: 138665; 8.5% error; agarose-fp
Quality coverage: 9.50x in Q20 bases; sum-of-contigs Quality
coverage: 10.56x in Q20 bases; agarose-fp
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54503 54602: gap of 100 bp
54603 99405: contig of 44803 bp in length
99406 99505: gap of 100 bp
99506 152947: contig of 53442 bp in length
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fragment_chain:1"
99506. .152947
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fragment_chain:1"
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33896 c 32934 g 39628 t :
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VERSION
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* consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.

* 1 16618: contig of 10618 bp in length

* 16619 16718: gap of 100 bp

1 194215: contig of 177497 bp in length.
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                                                                                                                                                                                                                                                                                                                              Assembly program: XCAP4; version 4.5 sequencing vector: plasmid; LO8752; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads consensus quality: 192819 bases at least Q40 consensus quality: 193115 bases at least Q30 consensus quality: 193125 bases at least Q20 consensus quality: 193255 bases at least Q20 Insert size: 194215; sum-of-contigs Insert size: 193590; 7.2% error; agarose-fp quality coverage: 9.54x in Q20 bases; sum-of-conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JAN-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced g1:17402315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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             Eukaryota; Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh 1 (bases 1 to 1119)
Duecker, K. and Scharm, B.
G-protein coupled receptor and dna se Patent; WO 010429-A 1 18-JAN-2001; MERCK PATENT GmbH (DE)
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Kato,S. and Kimura,T.
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Sequence 1 from Patent EP1090926.
AXI38829
AXI38829.1 GI:14274570
                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    Human g-protein coupled receptor
Patent: EP 1090926-A 1 11-APR-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
                                                                                     Harland, L.
                                                                                                                                                                     human.
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GVLMVMVLLAGANCVLDPLVYYFSAEGFRVTLRGLGTPHRARTSATNGTRAALAQSER
SAVTDDATRPDAASGGLLRPSDSHSLSSFTQCPQDSAL"
4 420 c 340 g 217 t
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RPSRCRYRDLEVRLCFESFSDELMKGRLLPLYLLAEALGFLLPLAAVYYSSGRVFWTL
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/db_xref="taxon:9606"
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1 (bases 1 to 1119)

White, K. E., Evans, W. E., O'Riordan, J. L., Speer, M. C., Econs, M. J., Lorenz-Depiereux, B., Grabowski, M., Meitinger, T. and Strom, T. M. Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23
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G protein-commission
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/db_xref="taxon:9606"
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Lee, D. K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F. Discovery and mapping of ten novel G protein-coupled regene 275 (1), 83-91 (2001)
                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1119)
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/protein_id="CAC03715.1"
/db_xref="GI:9843746"
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Matches
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                                  cctccctgcctggagcaccgctgg 545
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Lee,D.K., Nguyen,T., Lynch,K.R., (Lewis,T., Evans,J.F., George,S.R.
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GVLMVMVLLAGANCVLDPLVYYFSAEGFRNTLRGLGTPHRARTSATNGTRAALAQSER
SAVTTDATRPDAASQGLLRPSDSHSLSSFTQCPQDSAL"
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/protein_id="AAL26483.1"
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AX168124.1
                                                                  AX352473
Sequence
AX352473
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Patent: WO 0142288-A 42 14-JUN-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
      Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1720) Kato,S. and Kimura,T. Human proteins having hydrophobic domains and dnas e
                                                                       Patent: WO 0102563-A 25 11-JAN-2001;
SAGAMI CHEMICAL RESEARCH CENTER (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel proteins and nucleic acids encoding Patent: WO 0190187-A 25 29-NOV-2001; Curagen Corporation (US)
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/db_xref="taxon:9606"
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1; Mismatches 20
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Sequence 9 1
AX305129
AX305129.1
            and Au-Young, J.
G-protein coupled receptors
Patent: WO 0187937-A 9 22-NOV-2001;
Incyte Genomics, Inc. (US)
                                                                      Patterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M., Graul, R., Khan, F.A., Gandhi, A.R., Walia, N.K., Nguyen, D.B., Hafalia, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A.,
                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                  Homo sapiens
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nomics, Inc. (US)
Location/Qualifiers
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/db_xref="GI:12578461"
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Patent WO0187937
                                                                                                                                   Chordata;
Primates;
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Pred. No. 0.68;
1; Mismatches 20
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGTGGACCGCTACGCCGCCATCGTGCACCCGCTGCGACTGCGCCACCTGCGGCGGCCCC
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Sequence 19 :
AX128511
AX128511.1 (
                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrh.
1 (bases 1 to 2480)
Vogeli,G., Wood,L.S. and Merchant,K.
G protein-coupled receptors expressed Patent: WO 0131014-A 19 03-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                  human
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 7474|
a 803 c 640 g 555
/translation="MLANSSSTNSSYLPCPDYRPTHRLHLVYYSLYLAAGLPLNALAL
WVFLRALRVHSVYSYYMCNLAASDLLFTLSLPVRLSYYALHHWPFPDLLCQTTGAIFQ
MNMYGSCIFLMLINVDRYAAIVHPLRLRHLRRPRVARLLCLGVWALILVFAVPAARVH
                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
42. .1160
                                            /protein_id="CAC38940.1"
/db_xref="GI:14134979"
                                                                       /codon_start=1
                                                                                      /note="unnamed protein product"
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                                                                                                                                                            ocation/Qualifiers
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: WO0131014.
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nes 223; Conserv
CE 1 (bases 1 to 24580)

RS MIZNY,D.M., Adams,C., Balley,M., Barbaria,J., Blankenburg,K.,

RS MIZNY,D.M., Adams,C., Boxle,S., Brooks,A., Buhay,C., Bunac,C.,

Bodota,B., Bouck,J., Bowle,S., Brooks,A., Buhay,C., Bunac,C.,

Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,

David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,

David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,

Dugan-Rocha,S., Durbin,K.J., Fernandez,G., Ferraguto,D.,

Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,

Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,

Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,

Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,

Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,

Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,

Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,

Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L.,

Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,

Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gatgaccctgctcgcttcatcgtggtgcccgcggcctatgccttggcactgggcctgggg 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243000 pp DNA linear HTG 01-SEP-2000 Homo sapiens chromosome 12 clone RP4-761J14, RP11-433J6, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces. AC079387 AC005087 AC007438 AC005086 AC079387.1 GI:9961230
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ARPDATOSORRRKTVRLLLANLVIFLLCEVPYNSTLAVYGLLRSKLVAASVPAADRVR
GVLMYMVLLAGANCVLDPLYYYFSAEGFRNTLRGLGTPHRARTSATNGTRAALAQSER
SAVTTDATRPDAASQGLLRFSDSHSLSSFTQCPQDSAL*
a 759 c 622 g 592 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
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* This record will be updated with the finished sequence

* This record as it is available and the accession number will
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Center project name: J-31
Center clone name: RP4-761J14, RP11-433J6
Center clone name: RP4-761J14, RP11-433J6
Center clone name: RP4-761J14, RP11-433J6

Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 92% of reads
Chemistry: Dye-terminator Big Dye: 7% of reads
Chemistry: Dye-terminator Big Dye: 7% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 214565 bases at least Q40
Consensus quality: 230283 bases at least Q30
Consensus quality: 240000 bases at least Q20
Estimated insert size: 29807; agarose-fp estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary.
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be preserved
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                                                                                                                        Submitted (24-DEC-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUL 13, 2000 this sequence version replaced gi:6970649. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens clone RP11-21D12, LOW-PASS SEQUENCE SAMPLING
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                               Direct Submission
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                     Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.
                                                                            Center code: WIBR
                                                                                               Center: Whitehead Institute/ MIT Center for Genome
Project Information
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Center project name: L3982
Center clone name: 21_D_12
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**20606: gap of 864 bp in length 20607 21487: contig of 881 bp in length 21488 21587: gap of 100 bp 21488 22582: gap of 100 bp 23476 23575: gap of 100 bp 23576 24475: contig of 893 bp in length 2476 24575: gap of 100 bp 24576 2573: gap of 100 bp 2574 25573: gap of 100 bp 2574 26572: gap of 100 bp 2574 26573: contig of 878 bp in length 27451 27550: gap of 100 bp 27551 28440: contig of 878 bp in length 27451 27550: gap of 100 bp 27551 28440: contig of 87551 27550: gap of 100 bp 27551 28440: contig of 87551 27550: gap of 100 bp 27551 27550: gap NOTE: This record contains 141 individual sequencing reads that have not been assembled into sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will þe 878 977: gap of 100 bp
978 1861: contig of 884 bp in length
1862 1961: gap of 100 bp
1962 2860: contig of 899 bp in length
2861 2960: gap of 100 bp
2961 3820: contig of 860 bp in length
3821 3920: gap of 100 bp
3921 4784: contig of 864 bp in length 10671 10770: gap of 100 bp 10771 11658: contig of 888 bp 11659 11758: gap of 100 bp 11759 12654 12753: gap of 100 bp 12654 12753: gap of 100 bp 13648 13747: gap of 100 bp 13748 14729: gap of 100 bp 14630 14729: gap of 100 bp 14590 15598: contig of 882 bp 14730 15598: contig of 885 bp 15584 16683: gap of 100 bp 15584 16683: gap of 100 bp 15584 16683: gap of 100 bp 15684 16683: gap of 100 bp 15684 16683: gap of 100 bp 16584 16683 166 16584 16683: gap of 100 bp 11684 17579; contig of 896 bp in 16 17580 17679; app of 100 bp 17580 17679; app of 100 bp 17680 18563: contig of 884 bp in 16 18564 18663: gap of 100 bp 18564 18662; gap of 100 bp 19543 19642; gap of 19543 19642; gap of 100 bp 19543 19642; gap of 100 bp 19543 1964 6881 7754: contig of 874 bp
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, G., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                   2 (bases 1 to 125020)
Holmes, S.E., Ingersoll
Direct Submission
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MSAYCSCRKCKSKRCSGCMRCSWYCWYKCMRYGSWRMYKCCMSYKTCKYK 51112
                                                                                                                                                          SRRRMKGSAMRGMKCYCYTSSMRSTKSRSMKSSWRWGSKCYYCYGYWSCTKMRSMGCSYS
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                                 ccacggtggccttcgcggccgccttcctgctggtgctcgcggccaacgtg
                                                                                                              tggcgggcctggccctccctgcctggagcaccgctgggcaagctcggggctggcctccg 567
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                                                                             {\tt TGGSSMKCMGKYCCWGAGRSSRYCKSGSRMSMAGGSMSASMSMGKMTSGMSGRCCARSGR}
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l similarity 9.8%;
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/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
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NGAKYEGTWSNGLQDGYGTETYSDG"
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32731 c 30696 g 28283 t 4254 others
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/gene="JPH3"
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/note="isolated from a patient with Huntingt
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/db_xref="taxon:9606"
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Disease-Like 2 (HDL2)"
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Search completed: July 13, 2002, 02:12:56 Job time: 11715 sec

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Streptomyces nours	Streptomyces nours	Nucleotide sequenc	Sequence encoding	Rianodin receptor	Micromonospora DNA	Human transcriptio	Brn-3a polynucleot	Streptomyces clavu	S. clavuligerus cl	Streptomyces clavu	HSV-2 strain SB5 C	Human enzyme-relat			Human enzyme-relat		adenosine	Human adenosine re	Human low adenosin			Human protease-act		low adenosi		GTP-bindir	Human digestive sy	w.	Human P2YLi DNA.	Human CON217 G pro		Human protein HP03	Human cDNA encodin	Human G-protein co	Human DNA for pote	

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ALIGNMENTS

AAZ95039 RESULT CDS G protein coupled receptor; human; signal transduction; anaemia; neutropenia; thrombocytopenia; diagnosis; antidanaemic; immunostinulant; haemostatic; ophthalmic; antidiabetic; cerebroprotective; neuroprotective; nootropic; gene therapy; ss. 16-OCT-1998; 18-OCT-1999; Homo sapiens Human G protein coupled receptor 15334 cDNA. 15-AUG-2000 AAZ95039; AAZ95039 standard; (MILL-) MILLENNIUM PHARM INC 27-APR-2000. WO200023588-A2 18-OCT-1999; ш (first entry) 98US-0173869. 99US-0173869. 99WO-US24368 Location/Qualifiers 137..1255 /*tag= CDNA; 2559 ВP

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nes 224; Conserv
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gccgcccgcgtgcacaggccctcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.9%;
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Pred. No. 0.00023
1; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; hydrophobic domain; immune deficiency; autoimmune disorder; allergy; tissue growth; regeneration; wound healing; burn; tumour; periodontal disease; thrombolytic condition; haemostatic condition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human proteins (AAB61608-AAB61617) and their coding sequences (AAF28679-AAF28698). The proteins of the present invention have hydrophobic domains and can be used for the treatment of various immune deficiencies and disorders, such as severe combined various immune deficiencies and disorders, such as severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human proteins with hydrophobic domains, useful for the treatment of immune disorders, tumors, allergic conditions, thrombosis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Pages 116-117; 153pp; English
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                                                                                                                                                                                                                                                        Sequence 1116 BP; 141 A; 420
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PROTEGENE IN
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                                                          applicable in diagnosis and developing central nervous system, digestive organ
                                                                                                                                                                                                                                                                                                                                                     Key
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  This sequence
                          Claim
                                                                                                           P-PSDB;
                                                                                                                                                                                            12-APR-2000; 2000JP-0110761
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                                                inflammation,
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                                                        brain-originated G protein-coupled receptor protein TGR4, cable in diagnosis and developing drugs for diseases of e.g. al nervous system, digestive organs, immunological diseases,
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represents cDNA encoding
                         92;
                                                cancer and diabetes
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/product= "Human TGR4"
/note= "No stop codon
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                                                             ulcer; benign prostatic hypertrophy; migraine; vomiting; schizophrenia; psychotic disorder; neurological disorder; depression; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; vaccine; ss.
                                                                                                                Human; P2Y-like protein; 7 transmembrane receptor; AXOR17; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; stroke; Parkinson's disease; acute heart failure; hypertension; hypotension; urinary retention; osteoporosis; angina pectoris; myocardial infarction;
                               Homo
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                                                                                                                                                                                                                                                                               AAA64367;
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Pred. No. 0.00046;
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated AXOR17 polypeptide is useful for diagnosis and treatment of microbial infections and diseases e.g. cancer, schizophrenia, diabetes, obesity, stroke and myocardial infarction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotension, urinary retention, osteoporosis, angina pectoris, stroke, myocardial infarction, ulcers, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders including schizophrenia and depression and dyskinesias e.g. Huntington's disease or Gilles de la Tourette's syndrome. Antibodies to AXOR17 can also be used to treat these diseases. They can also be used in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 32; 35pp; English.
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30-APR-1999;
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                 agcgtgtgccgctgcggcttcgtacgcggtcccgggcccagggcggctgcccgcctggcc
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aacgtggaccgctacgccgccatcgtgcacccgctgcgactgcgccacctgcggcggccc
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; Pred. No. 0.000
1; Mismatches
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29-SEP-1999;
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01-OCT-1999;
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28-MAY-1999;
28-MAY-1999;
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28-MAY-1999;
29-JUN-1999;
29-SEP-1999;
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12-MAR-1999;
12-MAR-1999;
28-MAY-1999;
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                Claim 5; Page 46-47;
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                                Novel human orphan G protein-coupled receptors and for use in the identification of G protein-coupled
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                                                                                                    PHARM INC
                                                                                                                  99US-0157294.
99US-0416760.
99US-0417044.
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99US-0137127.
99US-0137131.
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99US-0123946
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               102pp; English.
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                                 receptor
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The

present sequence

is a

cDNA encoding hARE-4, an

endogenous human

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                                                                                          Human; G protein coupled
identification; agonist;
                          WO200022131-A2
                                                    Homo sapiens.
                                                                                                                                   Human
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27 AUG-1999
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12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
                                                                                                                                                                                                                                          of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used the exemplification of the present invention.
                                                                                                                                                                                                                                                                                               The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR). More specifically the present invention relates to non-endogenous, constitutively activated versions
                                                                                                                                                                                                                        Sequence 1119
                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic age
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antidiabetic; hypertensive; neuroleptic; antimigraine; asthma; cance cerebroprotective; tranquiliser; nootropic; anticonvulsant; vaccine;
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            The present cDNA sequence encodes human ICSR-1 protein which is a member of G-protein coupled receptor (7 transmembrane receptor) family. This receptor is expressed in either human embryonic kidney 293 (HEK 293) cells or adherent dfhr CHO cells. ICSR-1 is useful for treating and diagnosing infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain,
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                                                                                                                                                                                                                                                               Duecker K,
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    bulimia,
    asthma, Crohn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acute heart failure, hypotension, hypertension, urinary retent
osteoporosis, angina pectoris, myocardial infarction, stroke,
allergies, benign prostatic hypertrophy, migraine, vomiting, i
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RESULT
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Human G-protein coupled receptor PF1-004 DNA.
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                                               (first entry)
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obesity; diabetes; metabolic disease; neurological disease; inflammat psychotherapeutic; urogenital disease; tissue repair; dermatology; skin pigmentation; photoageing; osteoporosis; cardiovascular disease; agastrointestinal disease; infection; allergy; respiratory disease; pastrointestinal disease; infection; allergy; respiratory disease; G-protein coupled receptor; PF1-004; chromosome 12p13.3; disorder; sleep disorder; hair loss; inflammation;

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DB; AAB81125.
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1..1119
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                                                                                                                                                                                                                                                    Score 66; DB 22; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                    340 G;
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ggcctggcccggaggccgcctgccac
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AAS98045
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antisense probes), a host cell comprising an expression vector the GPCR sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds whi
                                                                                           nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes). A host call comments.
                                                                                                                                                                                                                                                               Disclosure; Page 113-114; 144pp; English
                                                                                                                                                                                                                                                                                                                                                 Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                         eptor polypeptides useful for :
  treating Alzheimer's disease,
erosis, stroke -
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AAS98085/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                    Human DNA for potential G protein-coupled receptor #42.
                                                                       12-MAR-2002
                                                                                                                                                   AAS98085 standard;
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 Human; G
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mes 223; Conservative
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                                                                     (first entry)
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 receptor;
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Pred. No. 0.00046;
1; Mismatches 207
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GPCR;
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GAL4;
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112 gatgaccctgctcgcttcatcgtggtgcccgcgggcctatgccttggcactgggcctgggg 171

Matches Query Match Best Local

223;

Conservative

۳.

Mismatches

207;

13;

Gaps

2

Similarity

10.7%;

Score 66; Pred. No.

DB 24; 0.00046;

Sequence 1237 BP;

243 A; 366 C;

463

G; 165

T; 0

other

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CC nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including CC antisense probes), a host cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides. The CC and methods of identifying modulators of the polypeptides. The CC polypeptides are useful for identifying modulator against the polypeptides. The CC polypeptides are useful for identifying modulator compounds which CC function as modulators, activators, repressors, agonists or antagonists of the novel GPCR polypeptides including the GAL4 polypeptide. The CC antibodies and nucleic acid probes as described above can be used to diagnose a variety of diseases or disorders in which GPCRs are involved e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, chronic obstructive pulmonary disease, Crohn's disease, epilepsy, macular degeneration, lymphoma, melanoma, cardiomyopathy, componession, epilepsy, macular degeneration, lymphoma, melanoma, componession, epilepsy, macular degeneration, lymphoma, melanoma, cut uberculosis and many other diseases listed in the specification. The composes and antibodies are also useful for diagnosing cognition and memory disease. Preferably, compounds that decrease or increase alzohion activity disease. Preferably, compounds that decrease or increase alzohion of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is cardiomyopathy.
psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obesity; diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cachondrosarcoma; chronic obstructive pulmonary disease; Croh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are for treating Alzheimer's disease, psoriasis, melanoma, multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 72; 144pp; English
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                                                             techniques. The
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2000US-205945P
                                                             present sequence is a novel GPCR polynucleotide of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; G-protein coupled receptor-3; GCREC-3; gene therapy; cirrhosis; transgenic animal; proliferative discorder; actinic keratosis; hepatitis nephrotropic; cancer; breast; bladder; bone marrow; brain; uterus; leukaemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy; stroke; neurological discorder; Alzheimer's disease; Parkinson's disease; nausea; meurological discorder; Alzheimer's disease; Parkinson's disease; nausea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein coupled receptor-3 (GCREC-3) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD08837
                                                                                                                  WO200142288-A2
10-DEC-1999;
22-DEC-1999;
                                               07-DEC-2000; 2000WO-US33382
                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                     disorder; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
99US-0172852
99US-0171732
                                                                                                                                              /product=
                                                                                                                                                                Location/Qualifiers
42..1310
/*tag= a
                                                                                                                                                  "Human GCREC-3 protein"
                                                                                                                                                                                                                                                                     nootropic; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646
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Query Match Best Local Similarity Matches 223; Conser

Conservative

10.7%;

Score Pred.

No ;

DB 22; 0.00046;

Length 1325;

Mismatches

207;

Indels

13;

Gaps

2

90

ctgccagccaacgtggcggccctggcaatgttcatccgcagcggcggcggcgcctgggccag gatgaccctgctcgcttcatcgtggtgcccgcggcctatgccttggcactggggcctgggg 171

ctcccctcaacgcgctagccct---ctgggtcttcctgcgcgcgctgcgcgtgcactcg

206

gtggtgagcgtgtacatgtgtaaccttggcggccagcgacctgctcttcaccctctcgctg

266 291

232 150 172

267 292 207

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Ω В Qy р Qy В δÃ 밁 QΥ 밁 Qy

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gcggccggggccacctactacgtgtccacctatgcggcggtggtcttcgccgcgctcatc 401

cccgttcgtctctcctactacgcactgcaccactggcccttccccgacctcctgtgccag

-ggcctggcccggaggccgcctgccac 341

acgacgggcgccatcttccagatgaacatgtacggcagctgcatcttcctgatgctcatc

386

387 402

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cDNA. GCREC is useful in somatic or germline gene therapy to correct a condensation of genetic deficiency, to express a conditionally lethal gene product and contract to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of GCREC. GCREC is also useful for generating hybridisation probes useful in mapping the naturally occurring genomic sequences and to create knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human diseases. GCREC is used to diagnose, prevent and treat proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis, hepatitis and cancer); cancer (breast, bladder, bone marrow, brain, cuterus cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma) neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's, Parkinson's disease, multiple sclerosis, dementia and other central nervous system disorders); cardiovascular disorders (angina pectoris, hypertension, atherosclerosis, congestive heart failure);
                                                             gastrointestinal disorders (dysphagia, peptic oesophagitis, oesophageal spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina, pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/
inflammatory disorders (acquired immunodeficiency syndrome (AIDS), Addison's diseases, allergies, anaemia, asthma, diabetes mellitus, atopic dermatitis, glomerulonephritis, Grave's diseases, osteoarthritis, parasitic, protozoal and helminthic infections) and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 160-161; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human G-protein coupled receptor polypeptides for diagnosing, preventing, and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-2000;
21-JAN-2000;
Sequence 1325 BP; 195 A; 473 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is human G-protein coupled receptor-3 (GCREC-3)
                                             osteoporosis, viral infections).
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2000US-0177331.
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403 G;
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25 -MAY - 2000;
28 - JUN - 2000;
19 - JUL - 2000;
                                                                                                                                                                                               18-DEC-2000;
26-FEB-2001;
09-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkitt's lymphoma; signal transduction pathway disorder; retinal disease; cell growth rate disorder; feeding disorder; control of feeding; obesity; starvation; fungal infection; noninsulin-dependent diabetes mellitus; bacterial infection; protozoal infection; viral infection; protozoal infection; viral infection; pain; cancer; anorexia; bulimia; asthma; parkinson's disease; acute heart failure; hypotension; urinary retention; osteoporosis; Crohn's disease; multiple sclerosis; Albright Hereditary Osteodystrophy; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; monic depression; delirium; dementia; severe metal retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
New polypeptide, useful for treating pain, cancer, urinary retention, osteoporosis, Crohn's disease, dyskinesias, acute heart failure, dementia, asthma and ulcer, comprises the isolated G-coupled
                                                                                                                                                                                                                                                                                                                                    24-MAY-2001; 2001WO-US17114.
                                                                                                                                                                                                                                        10-OCT-2000;
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25-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P2Y-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic disorder; cell signal processing disorder; metabolic pathway modulation disorder; chromosome 12p13.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autosomal dominant (2) Acrocallosal syndrome; dyskinesia;
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                                                         2002-106188/14.
DB; AAU11897.
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                                                                              u M, res ED, Alscares ED, Gangolli F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; GPCR9; G protein coupled receptor; disease; taste and scent detectability
                                                                                                                                                       CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmwembrane receptor.
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2000US-214372P.
2000US-219786P.
2000US-220593P.
2000US-239542P.
2000US-256402P.
2001US-271645P.
2001US-271699P.
2001US-275590P.
                                                                                                               Spytek KA,
Alsobrook
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                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "GPCR9"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                              Majumder K, Tchernev VT, JP, Burgess CE, Shimkets MacDougall JR, Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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                                                                                               Grosse WM;
RA, Taupi
Smithson G
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                                                                                                 Taupier
hson G;
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Query Match Best Local :

Similarity

10.7%;

Length 1560;

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cc retinal diseases including those involving photoreception, cell growth cc rate disorders, feeding disorders, control of feeding, potential cc obesity due to over-eating, potential disorders due to starvation, cc noninsulin-dependent diabetes mellitus, bacterial, fungal, protozoal and viral infections, pain, cancer, anorexia, bulimia, asthma, cc urinary retention, osteoporosis, Crohn's disease, multiple sclerosis, cc Albright Hereditary Osteodystrophy, angina pectoris, myocardial confirction, ulcers, allergies, benign prostatic hypertrophy, manic depression, delirium, dementia, severe metal retardation, autosomal cominant (2) Acrocallosal syndrome and dyskinesias, such as cominant (2) Acrocallosal syndrome and dyskinesias, such as completed of the coll signal processing and cometabolic pathway modulation. The present sequence encodes GPCR9 cometabolic pathway modulation. The present sequence encodes GPCR9 control of the coll signal processing and control of the coll signal processing and control of the coll sequence encodes GPCR9 control of the coll of the coll sequence encodes GPCR9 control of the coll of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and the polynucleotides encoding them. The GPCR, its encoding polynucleotide and an anti-GPCR antibody are useful for diagnosing polynucleotide and an anti-GPCR antibody are useful for diagnosing treating or preventing a GPCR-associated disorder in a human e.g. developmental diseases, immune diseases, taste and scent detectability disorder, Burkitt's lymphoma, signal transduction pathway disorders.
Sequence 1560 BP; 230 A; 561 C; 447 G; 322 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated G protein-coupled receptor related ypeptide (GPCR1a, 1b, 2, 3a, 3b, 4, 5, 6a, 6b, 7, 8a, 8b, and GPCR9) the polynucleotides encoding them. The GPCR, its encoding
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    other;
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Matches
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                               522 cctccctgcctggagcaccgctgg 545
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RESULT 1

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                autoimmune pulmonary inflammation, graft-versus-host disease and conditions, such as asthma and in regulation of haematopoiesis or lymphoid cell deficiencies. The proteins may also have utility in compositions used for bone, carrilage, tendon and/or nerve tissue growth or regeneration as well as wound healing and in the treatment of burns. The proteins may be used in the treatment of periodontal disease and in other tooth repair processes. Other uses include treatment of thrombolytic and haemostatic conditions, treatment or prevention of tumours and inhibiting infection by bacteria, viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human proteins (AAB61608-AAB61617) and their coding sequences (AAF28679-AAF28698). The proteins of the present invention have hydrophobic domains and can be used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention have hydrophobic domains and can be used for the treatmentarious immune deficiencies and disorders, such as severe combined immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; hydrophobic domain; immune deficiency; autoimmune disorder; allergy; tissue growth; regeneration; wound healing; burn; tumour;
                                                                                                                                                                                                                                                                                                                                         Sequence 1720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; thrombolytic condition;
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Pred. No.
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22-MAY-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor 1; cell proliferative disorder; arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammatory disorder; infection Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS
                                                                                                                                                              WPI;
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The invention relates
                               Claim
                                                                               neurological,
                                                                                          Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell prolife
                                                                                                                                                                                                         Patterson C, Lu
Khan FA, Gandhi
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DB; AAE16170.
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                                                                               treatment and preval, cardiovascular,
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2000US-207566P.
2000US-208834P.
2000US-208861P.
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Walia NK, Nguyen DB,
Reddy R, Kallick DA,
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human G-protein coupled receptor (GCREC)
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Tang
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Au-Young J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral meningitis, Creutzfeldt-Takob disease, schizophrenic disorders, amnesia, cardiovascular disorders such as arteriovenous fistula, atherosclerosis, hypertension, vascular tumours, myocardial infarction, hypertensive heart disease, infective endocarditis, cardiomyopathy, myocarditis; gastrointestinal disorders such as dysphagia, peptic oscophagitis, emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzhelmer's disease, Pick's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides and polynucleotides. GCREC polypeptides are useful for screening compounds that modulate their activity. They are useful the diagnosis, prevention and treatment of disorders which include
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Matches Query Match Best Local

Similarity

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Conservative

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Score 66; DB Pred. No. 0.00 1; Mismatches

DB 22; 0.00047;

Length 2480;

207;

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RESULT

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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                         The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit disorder, epilepsy, neuritis, neurostania, neuropathy, neurosis, Alzheimer's disease, parkinson's disease, migraine and senile
                      neurosis, Alzhelmer's disease, ratalisum subsequence procedures that dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present DNA sequence encodes human CON217 G protein-coupled receptor (GPCR) protein
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                                                                                                                                                                                                                                                                                                                              Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT 1 AI935035/c FEATURES COMMENT SOURCE ORGANISM JOURNAL source IMAGE Consortium (info@image.lln1.gov) for further Insert Length: 894 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 442. Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov AI935035 483 bp mwd17g08.x1 Soares_NFL_T_GBC_S1 Homo This clone is available royalty-free through LLNL; Tumor Gene Index NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap National Cancer Institute, Cancer Genome Ana Mammalia; Eutheria; 1 (bases 1 to 483) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens EST AI935035.1 GI:5673905 AI935035 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2328446"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B" mRNA sapiens Anatomy Project (CGAP), linear EST 17-DEC-1999 s cDNA clone ; contact the information.

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by Bento

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                                               Unpublished (1997)
Contact: Robert Strausberg, Femail: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                          BF195670 490 bp mRNA linear EST 03-NOV-2000 7n86g06.xl NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571762 3' similar to contains TAR1.tl TAR1 repetitive element;, mRNA
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.I
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: I
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange,
I.M.A.G.E. Consortium DNA Sequencing by: Washington Un
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                                                           mRNA sequence.
AI277080
AI277080.1 GI
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High quality sequence stop: 'Location/Qualifiers
Homo sapiens
Eukaryota; M
                                                                                                          AI277080
ql40h02.xl NCI_CGAP_C08
                                numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Clone="IMAGE:3571762"
/Clone_lib="NCI_CGAP_Ov18"
/clone_lib="NCI_CGAP_Ov18"
/tissue_type="fibrotheoma"
/lab_host="b|H0B (phage resistant)"
/rational cDNA was primed with a Not I - oligo(dT) primer [5'
rational cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
"block the county of the modified pT7T3 vector. Library
went through one round of normalization, and was
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/db_xref="taxon:
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2.3e-71;
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ggcccctccctgcctggagcaccgctgggcaagctcggggctg
                                                                       ccacgcggccggggccacctactacgtgtccacctatgcggcggtggtcttcgccgcgct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 978 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1874835"
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99.1%;
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Pred. No. 1.9e-69;
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cagctgtggctcacctactacctgggcctggcccggaggccgcgctgccacgcgggccgggg
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qk54f04.x1
similar to
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 460)
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                                                                                                                                                                                                                                                                                                                                                                   87
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                                                                                                                                                                                                                                                                                                                                                            /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1872799"
/clone_lib="NCI_CGAP_C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma"
/lab_host="DH10B"
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SW:P2Y4_HUMAN
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                                                                                                                                                                                                                                                                                73.9%;
99.3%;
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                                                                                                                                                                                                                                                                                Score 456.6;
Pred. No. 4.1
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Homo sapiens cDNA clone IMAGE:187279
N P51582 URIDINE NUCLEOTIDE RECEPTOR
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2;
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IMAGE:1872799 3'
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221
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KEYWORDS
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TITLE
Query Match
Best Local Similarity
Matches 447; Conserv
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7h17dl1.x1 |
similar to
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BF000091
BF000091.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Ilan Kirsch, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               info@image.llnl.gov
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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   Conservative
                                                                                           87
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3316245"
/clone_lib="NCI_CGAP_CO16"
/tissue_type="colon tumor, F
/lab_host="DH10B"
                                                                                      /note-Torgan: colon; vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made PCR-amplified cDNAs from a pool of 5,000 clones made made library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "a 150 c 172 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 bp mRNA linear EST 06-OCT-NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3316245 contains PTR5.t3 TAR1 repetitive element;, mRNA
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                 72.3%;
                 Score 446.6; DB Tend. No. 2.1e-67
   Mismatches
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GE:3316245 3'
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                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 358.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
1 (bases 1 to 392)
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                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 358 Location/Qualifiers
                 /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs; Soares NbHSF pool 1:
libraries and cloneIDs: 309384-310919, 323208-32
                                                                                                                                                                                                            /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:3525338"
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
    323208-325895 Soares
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BASE COUNT
ORIGIN
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AW072531/c
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ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtggctcacctactacctgggcctggcccggaggccgcgctgccacgcgggccggggccacc
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                                                                                                                                                                                                                                                                                                                                                                                                           AW072531 432 bp mRNA linear ES xa08e08.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567750 3' similar to contains PTR5.b2 TAR1 repe
                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (Dases 1 to 432)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                            Possible reversed clone: polyT not for Insert Length: 872 Std Error: 0.00
                                                                                                                                                                                              Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                element ;, mRNA sequence.
AW072531
                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                 human
                                                                               primer:
                                                               quality sequence stop: 432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8 9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bent Soares and M. Fatima Bonaldo."
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                Location/Qualifiers
1. .432
                                                                               -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                GI:6027529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 389.6; DB 1
Pred. No. 1.2e-57;
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                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ctgcctgcgccttcgcctggctggcgggcctggccctcccctgcctggagcaccgctggg 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgttcaacctggctctggttgatgagttcttcacgctcacgctgcagctgtggctcacc 306
                                                                                                                                                                                                                                                                                                                                                                               gcggtcccgggcccagggcggctgcccgcctggcccggtgcctacggbgccccgcgcgcg 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTACCTGGGCCTGGCCCGGAGGCCGCTGCACGCGC-----CGGGCCACCTATACGTGT 198
                                                                                                                                                                                                                                                              CAAGCTCGGGGCTGGCCT
                                                                                                                                                                                                                                                                                                                       CTGCCTGCGCCTTCGCCTGGCTGGCGGGCCTGGCCTCCCTGCCTGGAGCACCGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
418; Conserv
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
Tumor Gene Index
                                                                                                                                                        AW014139 333 bp mRNA linear IUI-H-BIO-aaj-b-07-0-UI.sl NCI_CGAP_Subl Homo sapiens
                                       Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 333)
                                                                                                                 EST
                                                                                                                             AW014139
AW014139.1 GI:5862896
                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung wbHL19w, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 72996-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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95.4%;
                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 385; DB 9;
Pred. No. 7.6e-57;
1; Mismatches 13
                                                       Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
             Anatomy Project (CGAP),
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                                                                       Euteleostomi;
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                                                                                                                                                                         cDNA clone
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Best Local Similarity
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214
                                  375 gcggcggttggtcttcgccgcgctcatcagcgtgtgccgctgcgggcttcgtacgcggtccc 434
                                                                                                                                    273
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                                                                                                                                                                                                                                                                    333 CCTGGCTATGGTTGATGAGTTATTCATGCTAACGCTGCAGCTGTGGCTCACATACTACCT
                                                                                                                                                                                                                                                                                                       gggcctggcccggaggccgcctgccacgcggccggggccacctactacgtgtccacctat 374
                                                                                                                                    GGGCCTGGCCCGGGGCCGCCT-CCACGCGGCCCGGGGCCACATAATACGTGACCACCTAT
GCGGCGGTGGTCTTCGCCGCGCTCATCAGCGTGTGCCGCTGCGGCTTCGTACGCGGTCCC
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Email: cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 236-273,

SCC_rich#Low_complexity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Subl library is a subtracted library derived from BI BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_CO4, NCI_CGAP_PT22, NCI_CGAP_PT28, NCI_CGAP_CO4, NCI_CGAP_EXI31, NCI_CGAP_EXI32, NCI_CGAP_EXI31, NCI_CGAP_EXI31, NCI_CGAP_EXI32, NCI_CGAP_BT22, NCI_CGAP_LU12, NCI_CGAP_BT22, NCI_CGAP_LU13, NCI_CGAP_BT22, NCI_CGAP_LU14, NCI_CGAP_LU13, NCI_CGAP_BT22, NCI_CGAP_LU14, NCI_CGAP_LU19, NCI_CGAP_BT22, NCI_CGAP_CO8, NCI_CGAP_LU14, NCI_CGAP_LU19, NCI_CGAP_BT22, NCI_CGAP_CO8, NCI_CGAP_LU14, NCI_CGAP_LU19, NCI_CGAP_GC4, NCI_CGAP_CO8, NCI_CGAP_LU14, NCI_CGAP_LU19, NCI_CGAP_GC4, NCI_CGAP_CO8, NCI_CGAP_LU14, NCI_CGAP_LU19, NCI_CGAP_GC4, NCI_CGAP_CO8, NCI_CGAP_LU12, NCI_CGAP_LU19, NCI_CGAP_GC4, NCI_CGAP_CO8, NCI_CGAP_LU12, NCI_CGAP_LU19, NCI_CGAP_GC4, NCI_CGAP_CO8, NCI_CGAP_LU19, NC
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/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 303.6; DB 9; Pred. No. 6.5e-43;
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UI-H-BIO-aai-a-07-0-UI.sl NCI_CGAP_Subl Homo sapiens
IMAGE:2709396 3', mRNA sequence.
AW014455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Cgapbs-r@mail.nlh.gov

Email: Cgapbs-r@mail.nlh.gov

Cligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 220)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/Clone=lib="NCLI CGAP_Subl"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Technologies)"
//note="vector: pT7T3D-pac (Pharmacia) with a modified
/note="vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site=1: wot | Site=2: Eco RI; The
RCI_CGAP_Subl library is a subtracted library derived from
BI constitutes a mixture of 21 normalized or
subtracted NCI_CGAP_Pr28, NCI_CGAP_RC010, NCI_CGAP_C016,
NCI_CGAP_Kid11, NCI_CGAP_LD2, NCI_CGAP_RC10, NCI_CGAP_LU5,
NCI_CGAP_LU24, NCI_CGAP_LD12, NCI_CGAP_RC04, NCI_CGAP_LU5,
NCI_CGAP_LU24, NCI_CGAP_LD12, NCI_CGAP_RC04, NCI_CGAP_GC6,
NCI_CGAP_LU24, NCI_CGAP_LD12, NCI_CGAP_RC04, NCI_CGAP_GC6,
NCI_CGAP_LU24, NCI_CGAP_LD13, NCI_CGAP_RC04, NCI_CGAP_GC6,
NCI_CGAP_LU24, NCI_CGAP_LD13, NCI_CGAP_GC6,
NCI_CGAP_LD25, These 21 libraries were pooled and a
single stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with a
driver whose composition is detailed below: NCI_CGAP_Kid3
pool 1 LLAM 3334-3337, 3682-3683, 3798-3803
(IMAGE
CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855)
NCI_CGAP_Kid3 pool 1 LLAM 338-3342, 3722-3725,
NCI_CGAP_LU35
NCI_CGAP_Kid3 pool 1 LLAM 338-3342, 3722-3725,
NCI_CGAP_LU35
NCI_CGAP_LU35
NCI_CGAP_CO10 pool 1 LLAM 3164-3167,
NCI_CGAP_PC20 pool 1
LLAM 337-2459, 2758-2759, 3062-3068
(IMAGE CloneIDs 125796-1258631,
NCI_CGAP_CO10 pool 1 LLAM 2644-2653, 2871-2872
(IMAGE
CloneIDs 1057416-1061255, 1144584-1145351) The resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2709396"
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                                                                                                                                                                                                                                                                       cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1030 row: e column: 21
                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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Subtraction was performed as previously described [Bonaldo Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB-NCI_CGAP_Lei2
TAG_LIB-NCI_CGAP_Lei2
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoR1;
Site_2: Xhoi; cDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5, adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (Universit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=AATCG"
81 c
                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4131836"
                                                                                                                           /clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
                                                                                                                                                                                                                         Location/Qualifiers
1. .1083
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94.1%;
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Pred. No. 3.5e-25;
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omo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gatgaacagcagtg-ttggggacctgggtgttggcggctgcagcctctggggatgaccctg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9999ccacctactacgtgtccacctat--gcggcggtggtcttcgccgcgcgctcatca-gc
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                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                               AW138178
AW138178.1 GI:6142578
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW138178 189 bp mRNA UI-H-BI1-acy-e-11-0-UI.sl NCI_CGAP_Sub3 IMAGE:2716124 3', mRNA sequence.
                                                                                                             www-bio.llnl
                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                  information can be found through the I.M.A.G.E. Consortium/LLNL at
                                                                                                                                                                                                                                                                                                                       (bases 1 to 189)
                                                                                           primer: M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies
a 363 c 318 g 184 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                      Location/Qualifiers
                                                                                                           .gov/bbrp/image/image.html
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78.2%;
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No. 7.1e-22;
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                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcgcggccg 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGTGTGCCGCTGCGGAGTCGTACGCGGTCTCGGGCCCAGGGCGACTGCCCAAATGGC
                                                                   fly), gen
                                                                                                                               CNSUU91P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                     AL053013.1 GI:4934461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_LOGAP_NCI_CGAP_Pr22, NCI_CGAP_KidS, NCI_CGAP_Kid11, NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL1, NCI_CGAP_LL2, NCI_CGAP_LL1, NCI
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                                                                                                            genomic survey sequence.
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TAG_TISSUE-germ cell
TAG_SEQ-AAATC"
a 66 c 69 g
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/clone_lib="WCI_CGAP_SUB3"
/clone_lib="WCI_CGAP_SUB3"
/lab_host="PH10B (Life Technologies)"
/lab_host="PH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_SUB3 library is a subtracted library the NCI_CGAP_SUB3 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 derived from BI. BI constitutes a mixture of 21
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Pred. No. 2.4e-15;
' wismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 CCCSCSSYCCSSSBSSSKCSSTSBSCSCCCSSKSVCGTSCSSSSSCSSSSSSSTSSSTSS 651
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                                                                                                                                                                                                                                                                                                                   gcccctccctgcctggagcaccgctgggcaagctcggggctggcctccgccacggtggcc 578
                                                                                                                                                                                                                                                                                                                                                                                                                 STSSSSTSWGSTSGSSSSSVGTSSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and AAron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RCI-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library can filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
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Drosophila melanogaster genome survey sequence T7 end of B BACR14N09 of RPCI-98 library from Drosophila melanogaster fly), genomic survey sequence.
AL066051
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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survey sequence T7 end of BAC
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                                                                                                                                                                                         CGCCGCCSCGCCCSCSSSSSCGSSCSSCSSCCSSSCCSSSGCCCGCCCSCGCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSGSSGCGSGCGSGSCCCCSGSCCCCSCSCGCSSCSCSCSCSCSCGCSCGCC 864
                                                                                                                          sceccecs
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                                                                                                                                                                                                                                                                                                                                 CGCCGGCSGGCGSSGCGGCSGGCCGSSCCGCSGKSKCGCGCGSGGSCSSSSGSGS
CNS006XK 935 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
                                     CNS006XK
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/db_xref="taxon:7227"
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223 ctgggccaggccctgcttctctacctgttcaacctggctctggttgatgagttcttcacg 282
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gcggccgccttcctgctggtgctcgcgg 609
                                                                                                                                                                                                                                        CGCSTSCSSSSCCSBBSYSTCSCTBCTKCSSGCSTGSGCTGCCGGGGGGGGGCGCGCGCGCGCG
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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na; Ephydroidea; Drosophilidae; Drosophila.
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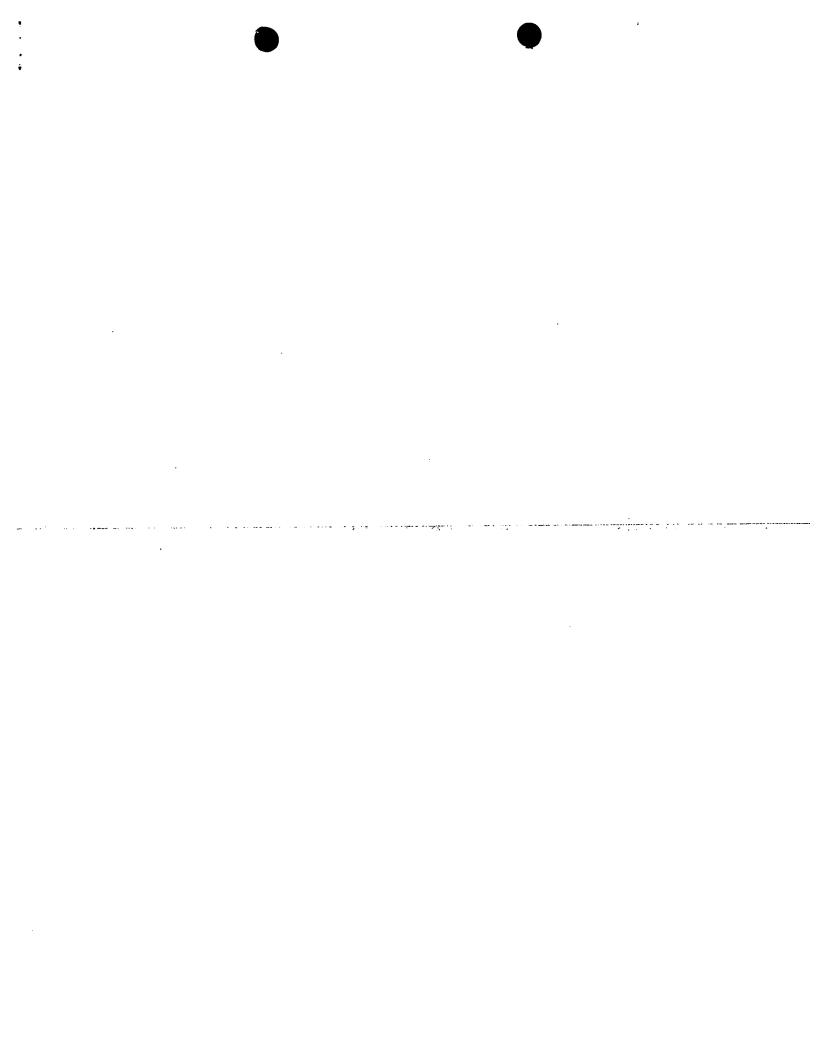
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371 ctatgcggcggtggtcttcgccgcgctcatcagcgtgtgccgctgcggcttcgtacgcgg
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                                                                                                                                                                                                                                       GGCBKGCKGGCGGGGGGGVCGRGGGSGGSGGSCGGSTGGCGGGKGGCGCKGCTSKGGCTGBGST
                                                                                                     acctgggcctggccggaggccgcctgccacgcgggccacctactacgtgtccac
                                                                                                                                                   GCGGGGGSKSGSGCSBGCGGGGSTKGGSGGGGSBSBTKYTBKGKGGCGGSSGSCCS
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Pred. No. 0.033;
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                                                                                                       GCSSCGCSCCCCSCCCCSSCGCSSSGCGGSGGCSSGCGSCGCGSCGGSGCGSC
                                                                                                                                                          SGGSGSGCCGGCSSCGCCSGCCCCSSGCSCCCCGCGCGSC-----GGSCCGCGCSCSG
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                           606
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Search completed: July 13, 2002, 01:37:09 Job time: 13040 sec

Page 11



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gb_htg:AC008737
gb_pr:HSU91939
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Database length: 1873333701
Search time (sec): 1815.170000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL-0.000 -LOOPEXT=0.000
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-FGAPOD=6.000 -GAPEXT=7.000 -YGAPOD=10.000 -YGAPEXT=0.500
-DELOD=6.000 -DELEXT=7.000 -YGAPOD=10.000 -YGAPEXT=0.500
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -TRR_SCORE=PCt
-TRANS=human40.cdi -LIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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924.76
927.e+03
285.46.64
1.4e+04
1.5e+04
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1 BC012755 Homo sapiens, clone N
1 BC012755 Homo sapiens, chrome N
1 BC01276 Macaca mulatta putati
1 AR096465 Sequence 5 from paten
1 AR096465 Sequence 6 from paten
1 AR096465 Sequence 2 from paten
1 AR096465 Sequence 1 from paten
1 AR096465 Sequence 2 from paten
1 AR096465 Sequence 1 from paten
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1 AX16812 Sequence 9 from paten
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0 | AC008737 Homo sapiens chromc
| U91939 Human putative G protei
| U91939 Human chromogranin A mF
                                                                                    ! AL132991 Streptomyces coelico
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                     X89271 H.sapiens mRNA for HG1
AR107256 Sequence 39 from pat
! AP001786 Homo sapiens genom
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gb_pat:E63120
gb_pr:HUMSOMATA
gb_pl:AP003418
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LOCUS AL3548
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                                                                                    misc_feature
                                                                                                                                                      misc_feature
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Mammalia; I
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seq_name: gb_htg:AL354876
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 152070 bases at least Q40
Consensus quality: 15218 bases at least Q30
Consensus quality: 15218 bases at least Q30
Consensus quality: 152484 bases at least Q20
Insert size: 138665; 8.5% error; agarose-fp
Quality coverage: 9.58x in Q20 bases; sum-of-contigs Quality
coverage: 10.56x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 1 clone RP11-244H3, PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bA244H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----Project Informatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jun 28, 2001 this sequence version replaced gi:13234889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved
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mmalia; Eutheria; Primates;
(bases 1 to 152947)
                                                                                                                                                                                                                                                                                                                     1 54502: contig of 54502 bp in length
54503 54602: gap of 100 bp
54603 99405: contig of 44803 bp in length
99406 99505: gap of 100 bp
99506 152947: contig of 53442 bp in length
Location/Qualifiers
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                                                                                       /note="assembly_fragment:02081
fragment_chain:1"
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                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="assembly_fragment:03694"
                                                                                                                                                                                       /clone="RP11-244H3"
/clone_lib="RPCI-11.1"
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2.5e+04
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, *** SEQUENCING IN
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E37240 Novel physiologicall
E63120 Peptide derivative.
L07833 Homo sapiens somatos
i AP003418 Oryza sativa gen
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alignment_block:
US-09-899-513-2 x AL354876/rev
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                                                     seq_documentation_block:
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194215 bp DNA linear HTG 30-JAN-2002 PROGRESS ***, 2 ordered pieces.
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Ratio: 5.459
milarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available the accession number will be preserved.

1 16618: contig of 16618 bp in length
16619 16718: gap of 100 bp
16719 194215: contig of 177497 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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/db_xref="taxon:9606"
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JOURNAL REFERENCE
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Kahn,M.L., Zheng,Y.W., Huang,W., Bigornia,V., Farese,R.V., Tam,C. and Coughlin,S.R. A dual thrombin receptor system for platelet (Nature (1998) In press 3 (bases 1 to 1534)
                                                                                            Kahn, M.L., Hammes, S.R., Botka, C. and Coughlin, S.R. Gene and locus structure and chromosomal localization protease-activated receptor gene family
                                                                   J. Biol. Chem. (1998) In press
2 (bases 1 to 1534)
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1534)
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CCGCCCTGGCACTGCCCCTGACACTGCAGCGGCAGACCTTCCGGCTGGCG
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alignment_block:
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APRGYPGQVCANDSDTLELPDSSRALLLGWVPTRLVPBALYGLLVLVGLLANGLALWVL
ATQAPRLPSTALLMULATADLLLALLPPRIAYHLRGQRWPTGEBACRLATAALYGHM
YGSVLLLAAVSLDRYLALVHPLRARALRGRRLALGLCMAAWLMAAALALPLTLQRQTF
RLARSDRVLGHDALPLDAQASHWQPAFTCLALLGCELPLLAMLLCYGAYLHTLAASGR
RYGHALRLTAVVLASAAHFVPSNLLLLLHYSDPSPSAMGNLYGAYVPSLALSTLNSC
VDPFIYYYVSABFRDKVVAGGLFQRSPGDTVASKASAEGGSRGMGTHSSLLQ"
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/db_xref="taxon:9606"
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/db_xref="GI:3396081"
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Sequence 1 from patent US 6111075.
AR108643
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Xu,W., Presnell,S.R.
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Homo sapiens protease-activated
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AF055917.1 GI:3293321
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Xu,W., Andersen,H., Whitmore,T.E., Presnell,S.R., Yee,D.P., Xu,W., Gilbert,T., Davie,E.W. and Foster,D.C. Ching,A., Gilbert,T., Davie,E.W. and Foster,D.C. Cloning and characterization of human protease-activated receptor Proc. Natl. Acad. Sci. U.S.A. 95 (12), 6642-6646 (1998)
                                                                                                                                                                                                                 Xu,W., Andersen,H., Whitmore,T.E., Gilbert, Foster,D.C.
Direct Submission
Submitted (26-MAR-1998) Biochemistry, University, NE Pacific Street, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                                  98283984
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'-Aersen.H., Whitmore,T.E.,
/notes"PAR4; member of family of G-prote: protease activated receptors //codon_start=1 //product="protease-activated receptor 4" //protein_id="AAC25699.1" //db_xref="GI:3293322"
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176. .1333
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/chromosome="19"
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Quality:

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US-09-899-513-2 x AX211769
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ProThr
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                                                                                                                                                                     AspGluPhePheThrLeuThrLeuGlnLeuTrpLeuThrTyrTyr.Leu. 105
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Ratio:
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495

90

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174 889 166 839

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653

603

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553

89

509

459

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989

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789

144

to: AX211769

from:

to: 4925

177.50 1.659 45.532

Percent Identity:

235 13 30.638

739

127

119 589 106 539

ProThr....

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ORQTFRLARSDRVLCHDALPLDAQASHWQPAFTCLALLGCELPLLAMILCYGATLHTL
AASGRRYGHALRITAVVLASAVAFFVPSINLLLHYSDPSPSAMGNLYGAYVPSIALS
TLNGCVDPFIXYYYSAFFPDRVRAGLFQRSPGDTVASKASAEGGSRGMGTH"
a 1582 c 1411 g 955 t
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                                                                                                                                                      Sequence update by submitter on Jun 19, 2001 this sequence version replaced gi:14389060. On Jun 19, 2001 this sequence version replaced gi:14389060. To cite this work please use: SeattleSNPs. NHLBI Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.mbt.washington.edu).
                                                                                                                                                                                                                                            Submitted (19-JUN-2001) Molecular Biotechnology, Washington, 1705 NE Pacific, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                Direct Submission
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Rieder, M.J., Carringt
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/frequency="0.02"
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414. .709
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RLARSDRVLCHDALPLDAQASHWQPAFTCLALLGCFLPLLAMLLCYGATLHTLAASGR
RYGHALRLTAVVLASAVAFFVPSNLLLLLHYSDPSPSAWGNLYGAYVPSLALSTLNSC
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join(1207. .1
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1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="mRNA spans determined /product="coagulation factor 1032 . 10742
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join(1032. .
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2560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="coagulation i
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/note=""""
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replace="G"
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replace="T"
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/frequency="0.02"
/replace="T"
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/replace="A"
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4587
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3327
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/replace="T"
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'replace="T"
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/replace="C"
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/replace="A"
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replace="A"
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alignment_block:
US-09-899-513-2 x AF384819
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1706 CCCACCAGG.....CTGGTGCCCGCCCTCTATGGGCTGGTCCTGGTGGT
1994 CTGGATCGCTACCTGGCCCTGCTGCACCCCTGCGGGCCCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                   1844 GACCTCCTGCCCTGCCCCTGCCCCCCGCGATCGCCTACCACCTGCG 1893
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                                                                                                                                                                                                                 2044 TGGCCGGCGCCTGGCCCTTGGACTCTGCATGGCTGCTTGGCTCATGGCGG 2093
                                                                                                                                                                                                                                                                                                                                                            1944 CACTCTATGGTCACATGTATGGCTCAGTGCTGCTGGCCGCCGTCAGC 1993
                                                                                                                                           2094 CCGCCCTGGCACTGCCCCTGACACTGCAGCGGCAGACCTTCCGGCTGGCG 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1800 CTCGGCTGCCCTCCACCATGCTG.....CTGATGAACCTCGCGGCTGCT
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                                                                                                                                                                                                                                     144 ValProGlyProGlyArgLeu..ProAlaTrp......
                                                                                                                                                                                                                                                                                                                                                                                                119 ProThr......ThrCysProProMetArgAr 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 lyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAlaLeuVal 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 ProAlaArgPheIleValValProAlaAlaTyrAlaLeuAlaLeuGlyLe
                                                                                                   yAlaProArgAlaLeuProAla.....
                                                                                                                                                                                                                                                                                                             gTrp.SerSerProArgSerSerAlaCysAlaAlaAlaAlaSerTyrAla 143
                                                                     CGCTCCGATCGCGTGCTCTGCCATGACGCGCTGCCCCTGGACGCACAGGC
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4988 .5133
/rpt_family="L1MD1"
/rpt_type=dispersed
4995
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/replace="C"
5980
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/replace="T"
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REFERENCE
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TITLE
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LOCUS AC008737
                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 26, 2001 this sequence version replaced gi:13752640.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces.
                                                                                                                                              estimation.
                                                                                                                                                                                                                                              estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 248680)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC008737 248680 bp DNA 1:
Homo sapiens chromosome 19 clone CTD-2538G9,
PROCRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 248580)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE2; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC008737.9 GI:15021998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 155094 155193: contig of 135093 bp in length 155094 155193: gap of unknown length 155194 248680: contig of 93487 bp in length.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2538G9"
                                                                                                                     Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 to 248680)
                                                                                                                                                                                                                                                             Consensus quality: 247465 bases at least Q40 Consensus quality: 247949 bases at least Q30 Consensus quality: 247983 bases at least Q20 Estimated insert size: 248980; agarose-fp estimation Estimated insert size: 248035; sum-of-contigs
                                                                                                 .248680
                                                                                                                                                                   Quality
                                                                                                                                                                                                             Quality coverage:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Center Project Name: 804726
Center clone name: CTD-2538G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                   coverage:
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                                                                                                                                                                                                                11.93 in Q20 bases; agarose-fp
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), *** SEQUENCING IN
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                                                                                                                                                                     sum-of-contigs
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seq_name: gb_pr:HSU91939
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ORIGIN
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                                                                     ..TrpProProArgTrpProSerArg...ProProSerCysTrpCys
                                                                                                                                                                                                                      TGCCCCTGCTGGCATGCTGCTGCTACGGGGCCACCCTGCACACGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTCTATGGTCACATGTATGGCTCAGTGCTGCTGCTGGCCGCCGTCAGC
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Gaps:
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SOURCE
ORGANISM
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US-09-899-513-2 x HSU91939
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Percent Similarity:
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                                                                                                CTGGCGGCCTTCGCCGGGCCTGCTGGGCAAC.....GCCTTTGTGGT
                                                                                                                                                                                                GTCCGGCCGGGACCTGCCCTACGGCTACGTCTACATCCCCGCGCTCTAC
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                                                                                                                             AlaLeuAlaLeuGlyLeuGlyLeuProAlaAsnValAlaAlaLeuAlaMe
                                            tPheIleArgSerGlyGlyArgLeuGlyGlnAlaLeuLeu...LeuTyrL
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-FEB-1997) Pharmacology, University of Taddle Creek Rd., Toronto, ON M5S 1A8, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 1400)
Jung, B.P., Nguyen, T., Kolakowski, L.F.
George, S.R. and O'Dowd, B.F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jung, B.P., Nguyen, T., Kolakowski, L.F. Jr., Lynch, K.R., Heng, H.H., George, S.R. and O'Dowd, B.F.
Discovery of a novel human G protein-coupled receptor gene (GPR25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1400)
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Human putative
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FCYCRISRRLRRFRRFAIESTFVGSWLPFSALEALFI
FCYCRISRRLRRPPHVGRARNSLRIFAIESTFVGSWLPFSALEALFI
FCYCRISRRLRRFRRFAIESTFVGSWLPFSALEALFI
FCYCRISRRLRRFRRFAIESTFVGSWLPFSALEALFI
FCYCRISRRLRRFRRFAIESTFVGSWLPFSALEALFI
FCYCRISRRLRRPPHVGARNSLRIFAIESTFVGSWLPFSALEALFI
FCYCRISRRLPRTFTTFVGSWLPFTAITTFVGSWLPFTAITTFVGSWLPFTAITTFVG
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50.943
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/map="1q32.1"
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AUTHORS
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Konecki,D.S., Benedum,U.M., Gerdes,H.H. and Huttner,W.B.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pheochromocytoma. cDNA to mRNA, (library of J.Mallet), clone hCgA/42.
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                                                                                                                                                                                                                                                                                                                                                       copy of sequence for [1] kindly
/codon_start=1
/protein_id="AAA52017.1"
/db_xref="GI:180527"
                                                            /note="chromogranin A precursor"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                   /product="chromogranin
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alignment_block:
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aTrp.....ProGlyAlaTyrGlyAlaProArgAlaLeuProAla.... 165
                                                 GCGGCCCAGGGCCCCTGAAGCCGTAGGCCCCGGGCCCCGGAAGGAGCTTC 1198
                                                                                                  AlaAlaSer.....TyrAlaValProGlyProGlyArgLeuProAl 152
                                                                                                                                                     GTCCTCCCGGGAGGATG......GCCTCCAGCCTCGTCGCAGCT 1248
                                                                                                                                                                                               ysProProMetArgArgTrpSerSerProArgSerSerAlaCysAlaAla 138
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KRSPMPVSQECFETLIGDERILSILRHONLLKELQDLALQGEAKERAHQQKKHSGFED

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vien, C., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerThrAlaGlyGlnAlaArgGlyTrpProProProArgTrpProSerAr 195
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Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC027113 159391 bp DNA linear HTG 25-MAY-
HOMO sapiens chromosome 5 clone RP11-67212 map 5, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 25, 2000 this sequence version replaced g1:7656748 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 672_1_2

Center clone name: 672_1_2

Sequencing vector: M13; M77815; 100% of rechemistry: Dye-terminator Big Dye; 100% of Assembly program: Phrap; version 0.960731

consensus quality: 149154 bases at least Consensus quality: 154165 bases at least Consensus quality
                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (26-MAR-2000) Whitehead Institute/MIT Center for 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- Genome Center
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               t least Q40
t least Q30
                                                                                                                                                                       of reads
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 195000; agarose-fp
Insert size: 157491; sum-of-contigs
Quality coverage: 4.2 in Q20 bases;
Quality coverage: 5.2 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 156049 bases at least
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1474 3371:
3372 3471: gap
                                                                                                                                                                                                                                                                                                                     278 135377: gap of
                                                                                                                                                                              /clone="RP11-67212"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                   109528: gap of
                                                                                                                                                                                                                                                                                                                                                                                                             80007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61546: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52895:
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                                                                                                                                                                                                                                                                                                         159391:
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                                                                                                                                                                                                                                                                                                                                     135277:
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'1: gap of 100 bp
5991: contig ~f ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52795: contig of 9458 bp in 95: gap of 100 hr
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27394: contig of 4127 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8001: contig of 1910 bp in length
11: gap of 100 bp
10452: contig of 2351 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61446: contig of 8551 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1373:
                                               .10452
                                                                                                         .5991
                                                                           .8001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
(167: contig of 5767 bp
: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yap of 100 bp 100 to 100 bp 101 contig of 2520 bp in length 100 bp
                                                        assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                        ap of 100 bp:
contig of 10985 bp in length
                                                                                                                                                                                                                                                                                                                                                              p of 100 bp
contig of 18325 bp in
                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp
contig of 10996 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p of 100 bp contig of 4447 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp
contig of 4826 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 3701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 1373 bp in length of 100 bp
                                                                                                                                                                                                                                                                                                      contig of 24014 bp in length
                                                                                                                                                                                                                                                                                                                                  contig of 25749 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
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sum-of-contigs
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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132433 ATGG...CCTCTGCAAGCTCAGCAGCTTCGCGCTGGCGGGCACGCGCTGC 132479
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                                  116 oGlyProProThrThrCysProProMetArgArgTrpSerSerProArgS 133
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                                                                                                        TrpLeuThrTyrTyrLeuGlyLeuAlaArgArgProProAlaThrArgPr 116
                                                                                                                                               TGCTGCACCTGGCGGCAGCTGACCTGGGCTTCGTGCTCACGCTGCCGCTG 132389
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Homo sapiens chromosome l clone RP11-180A14, complete sequence.
AC099756 AL356097
AC099756.2 GI:18369993
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Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-JAN-2002) Genome Center, University of Washington, Box 352145, Seattle, MA 98195, USA on Jan 25, 2002 this sequence version replaced gi:17017615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-NOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 167302)
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Overlapping Sequences:
5': RP11-93N17 AL450104, 45836-bp overlap
3': RP11-168016 AL358473, 2000-bp overlap
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                                                                                           Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET; 92% of reads Chemistry: Dye-terminator Big Dye; 8% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 167134 bases at least Q30 Consensus quality: 167259 bases at least Q20 Consensus quality: 167292 bases at least Q20 Insert size: 167302; sum-of-contigs Quality coverage: 12.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                 Center clone name: RP11-180A14 (sc0650)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file. zero.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by Aschalica. fragments are separated by dashed lines. ECORI

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Location/Qualifiers 1167302 /organism="Homo sapi./db_xref="taxon:9606 /chromosome="1" /chomosome="11:B0814" /clone="Rp11:B0814" /clone_lib="RPCI hum 37479 c 38785 g									2102	1825	<800	17015	7228	2472	3215	1233	8800	8211	2990	5822	1506	8800	1059	<800	<800
Location/Qualifiers 1167302 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="1" /chone="spl1-180A14" /clone="fb="RPCI human BAC library 37479 c 38785 g 47273 t									9551	6279	5851	975	5912	2188	4825	3361	1222	10028	3365	6231	2525	12123	12011	2429	43
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granin A mRNA, complete cds. 180528 A; parathyroid secretory protein 1. comocytoma, cDNA to mRNA, clone pGHCGA. stazoa; Chordata; Craniata; Vertebrata; theria; Primates; Catarrhini; Hominidae; to 1811) Ahn,T.G., Levine,M.A., Allison,A., Cohe Cohn,D.V. and Israel,M.A.	seq_documentation_block: IOCUS HUMCHRAA 1811 bp mRNA linear PRI 01-NOV-1994	CGGCGAGGAGCCC	lyTrpProProProArgTrpProSerArgProProSerCysTrpCys		177 aTroSerThrAlaGly	164ProAlaProSerProGlyTrpArgAlaTrpProLeuProAl 177	55581 GGTGAAGCTGCGCGAGGCCACCCCGCGCTGG 55630	150 LeuProAlaTrpProGlyAlaTyrGlyAlaProArgAlaLeu 163	133 erSerAlaCysAlaAlaAlaAlaSerTyrAlaValProGlyProGlyArg 149 ::: ::: ::::::	55484 ATGGCCTCTGCAAGCTCAGCAGCTTCGCGCTGGCGGGCACGCGCTGC 55530	116 oGlyProProThrThrCysProProMetArgArgTrpSerSerProArgS 133		${\tt TrpLeuThrTyrTyrLeuGlyLeuAlaArgArgProProAlaThrArgPr}$		euPheAsnLeuAlaLeuValAspGluPhePheThrLeuThrLeuGlnLeu	67 tPheIleArgSerGlyGlyArgLeuGlyGlnAlaLeuLeuLeuTyrL 83 ::::::	55297 CTGGCGGCCTTCGCCGTGGGCCTGCTGCGGCAACGCCTTTGTGGT 55340	51 AlaLeuAlaLeuGlyLeuGlyLeuProAlaAsnValAlaAlaLeuAlaMe 67	55247 GTCCGGCCGGGGACCTGCCCTACGGCTACATCCCCGCGCTCTAC 55296	34 ysserLeuTrpAspAspProAlaArgPheIleValValProAlaAlaTyr 50	24 SerSerValGlyAspLeuGlyValGly	eg 1/1 to: AC099756 from: 1 to: 167302	us-09-899-513-2 x AC099756	Similarity: 53.500 Percent Identity:	Quality: 167.50 Length: 200 Ratio: 1.565 Gaps: 10

BASE COUNT ORIGIN

FEATURES source

alignment_scores:

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alignment_scores:
Quality:
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J. Biol. Chem. 263 (23), 11559-11563 (1988)
88298816
Draft entry and computer-readable sequence
by L.J.Helman, 31-MAY-1988.
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42.922
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LOCUS BC012755
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               /note="Vector: 23. .1009
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1245 GTCCT......CCCAGGAGTTCGGCCTCGAGCCTC
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                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
Series: IRAL Plate: 24 Row: m Column: 23
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1432 bp mRNA linear Homo sapiens, clone MGC:16126 IMAGE:3627785, mRNA, BC012755
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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1 (bases 1 to 1432)
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                                                                                                                                                                                                                                                                        passed the following selection
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                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                             Location/Qualifiers
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SerThrAlaGlyGlnAlaArgGlyTrpProProProArgTrpProSerAr 195
                                           CTCAGCCGTCAGCTCGTTGGCCAGCTGGTCCATCTTGCTCCAGCGTTTGG
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LAKELTAEKRLEGQEEEEDNNDSSMKLSFRAARYGFRGPGPOLRRGWAPSSREDSLEA
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1.758
42.466
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley.C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1674 bp mRNA linear PRI 12-JUL
Homo sapiens, Similar to chromogranin A (parathyroid secretory
protein 1), clone IMAGE:4127895, mRNA, partial cds.
BC009384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 26 Row: h Column: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC009384.1 GI:14424739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute, 31 Center Drive, Room 11A03, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  distribution:
                                                                                             /translation="GTROECFETLRGDERILSILRHQNLLKELQDLALQGAKERAHQOKKHSGFEDELSEVLENQSSQAELKEAVEEPSSKDVMEKREDSKEAEKSGEATDGARPQALPEPMQESKAEGNNQAFGEEEEEEATNTHPHASLFSQKYPGFPQAEBDSGLSQGLVDREKGLSAEPGWQAKREEEEEEEEARAHAFBEEBGPTVVLNPH9SLGYKEIRKGESRSEALAVDGAGKPGAEEAQDPEGKGEQEHSQQKEEEEEMAVVPQGLFRGGKSGELEGERSEALAVDGAGKPGAEEAQDPEGKGEQEHSQQKEEEEEDNRDSSMKLSFRARAYGFR
                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pOTB7" <1. .1224
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/db_xref="GI:14424740"
                                                                                                                                                                                                                                                                                                 /product="Similar to chromogranin A (parathyroid
protein 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Brain, ne
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4127895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to 1674)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.nisc.nih.gov/
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Primates;
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroblastoma"
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of Health Intramural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      information can be http://image.llnl.c
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                                                                                                                                                                                                                                                                                                                        secretory
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alignment_block:
US-09-899-513-2 x BC009384/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 163.50
Ratio: 1.758
Percent Similarity: 42.466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: BC009384 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1295 CAGGACCTGCCAAGGGGACAGCAGAGCCAGGGCACAGGGT...GCCCTG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1345 GCAGGCTGGAGGCTGCCTACCGGAAGCAGCGTCCGGGCCATCTGGC 1296
                                                                                                                                                                                                                                                                                                                                          1015 GCGGCCCAGGGCCCTGAAGCCGTAGGCCCGGGCCCGGAAGGAGCTTC 966
                                                                                                                                                                                                                                                                                                                                                                                                                            1053 GTCCTCCCGGGAGGATG......GCCTCCAGCCTCGTCGCAGCT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1177 .....CTGCCTCAATGGCCGACAGGCTCT 1154
                                                                                                                                                                                                                                                                                                                                                              139 AlaAlaSer......TyrAlaValProGlyProGlyArgLeuProAl 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ysProProMetArgArgTrpSerSerProArgSerSerAlaCysAlaAla 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 rArgPro......GlyProProThrThrC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1153 CCAGCTCCTGGTCTCTGGTCTGCGGTTTGCGCTGCCCTCCTCTTTC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 .....TyrTyrLeuGlyLeuAlaArgArgProProAlaTh 114
                          195 gProPro 197
                                                                                                                     179 SerThrAlaGlyGlnAlaArgGlyTrpProProProArgTrpProSerAr 195
                                                                                                                                                                    915 CTCAGCCGTCAGCTCCTTGGCCAGCTGGTCCATCTTGCTCCAGCGTTTGG 866
                                                                                                                                                                                                       166 .....ProSerProGlyTrpArgAlaTrpPro.....LeuProAlaTrp 178
                                                                                                                                                                                                                                                   965 ATGGAACTGTCCCGGTTGTCCTCCTCCTCCTCCCGCCCCTCCAGCCGCTT 916
                                                                                                                                                                                                                                                                                152 aTrp.....ProGlyAlaTyrGlyAlaProArgAlaLeuProAla.... 165
839 TCCTCCT 833
                                                                               865 AGT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 spaspProalaargPheIleValValProalaalaTyrAlaLeuAlaLeu 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 euValAspGluPhePheThrLeuThrLeuGlnLeuTrpLeuThr..... 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 ....ValGlyGlyCys......SerLeuTrpA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 219
Gaps: 12
Percent Identity: 31.507
                                                                                    CCTCCCACTCCTTGGAGAGCCGC 840
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Database length: 858457221
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Query length: 205
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV19863
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV19863
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA10298
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA50775-
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH43632
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-Q=-lgeneseq_032802 -QFMT=fastap -SUFFIX-p2n.rng -GAPOP-12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -XAPEXT=0.000
-QAAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-BELOP=6.000 -DELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DCALIGN=200 -THR_SCORE-pct
-TRANS=human40.cdi -LIST=45 -ALIGN=15 -MODE-LOCAL -OUTPMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
USER=US09899513_@CGN1_1_0 -NOPU=6 -ICPU=3 -LONGLOG
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Compugen Ltd.
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Sequence 1534

BP;

235

A; 526

ი; 479 G;

293 T; 1 other;

Quality:

Ratio:

177.50 1.659 45.532

Percent Identity:

235 13 30.638

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seq_documentation_block:
ID AAX90981 standard;
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                                                 involved in thrombin-mediated activation of platelets and other haematopoletic cells. It is used for screening novel thrombin agonists or antagonists. The agonists are used as therapeutics to treat wounds, promote clotting and as reagents to activate platelets in diagnostic tests. Antagonists are used to control blood coagulation, treat heart attacks and strokes, and block inflammatory and proliferative responses that occur in normal wound healing and variety of diseases including atheroscierosis, restenosis, pulmonary inflammation (ARDS) and
                                    glomerulosclerosis
                                                                                                                                                                                                 receptor 4 (PAR4) which is a thrombin receptor expressed on cell surface. PAR4 is activated by thrombin and mediates signalling events e.g. phosphoinositide hydrolysis, calcium efflux and platelet aggregation. The receptor is highly expressed in spleen cells and likely to be
                                                                                                                                                                                                                                                                                                                Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protease-activated receptor 4 (PAR4) cDNA.
                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding human protease-activated
                                                                                                                                                                                                                                                                                                                                                 compound assays for thrombin agonist and antagonist activity
                                                                                                                                                                                                                                                                                                                                                                    DNA molecules encoding protease-activated receptor 4, useful
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-619953/53.
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surfactant depletion; respiratory; bronchodilator; antlinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; pulmonary hypertension; emphysema; pulmonary transplantation rejection; cancer; ss. chronic obstructive Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; pulmonary disease; pulmonary infection; bronchitis;

Homo sapiens.

WO200062736-A2

26-OCT-2000

24-MAR-2000; 2000WO-US08020

06-APR-1999; 99US-0127958

(UYEC-) UNIV EAST (NYCE/) NYCE J W. CAROLINA.

Nусе JW

WPI; 2000-679539/66.

cancers and respiratory obstructions -Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g. ď for treating not

Disclosure; Page 1415; 1592pp; English.

Clung/respiratory disorders and malignancies, such as stimulating and cc activating peptide factors and transmitters, transcription factors, climmunoglobulins and antibodies, antibody receptors, cytokines and cc hamokines, endogenously produced specific and non-specific enzymes, commonkines, endogenously produced specific and their receptors, cytokines and cc hemokine receptors, adhesion molecules and their receptors, cytokine and cc nervous system (CNS) and peripheral nervous and non-nervous system and creceptors, CNS and peripheral nervous and non-nervous system cc receptors, CNS and peripheral nervous and non-nervous system entral creceptors, compounded to the compound of th immunosuppressive, antiasthmatic, hypotensive and cytostatic activities The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification o hypertension, emphysema, chronic obstructive pulmonary disease (COPD), can have respiratory, present invention. bronchodilator, antiinflammatory, analgesic, exemplification of

Sequence 1534 BP; 235 A; 526 C; 479 G; 293 T; 1 other

Percent Similarity: Quality: Ratio: 177.50 1.659 45.532 Gaps: Percent Identity: Length: 235 13 30.638

alignment_block:

Human low adenosine antisense oligonucleotide related sequence #2998

14-MAR-2001

(first entry)

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                                                                                                                                                                 _documentation_block:
AAA35309 standard;
Human; adenosine receptor; low adenosine antisense oli phosphorothicate; impaired respiration; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
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                                                     Human adenosine receptor related polynucleotide 2nd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 uGlyLeuProAlaAsnValAlaAlaLeuAlaMetPheIleArgSerGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                      TGCCCCTGCTGGCCATGCTGCTGCTACGGGGCCACCCTGCACACGCTG
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                                                                                                                                                                                                                                                                                                                                                              pSerThrAlaGlyGlnAlaArgGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......ProGlyAlaTyrGl 158
                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn·emb1/NA2000.DAT:AAA35309
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                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                          TGGCCTTCTTCGTGCCCAGCAACCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProSerProGlyTrpArgAlaTrp..... 173
                                                                                                                                                                   1534
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                 low adenosine antisense oligonucleotide
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                                                      SEQ ID NO:183.
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alignment_block:

Percent Similarity:

US-09-899-513-2 x AAA35309

Align seg

1/1

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AAA35309

from:

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228 CCCACCAGG.....CTGGTGCCCGCCCTCTATGGGCTGGTCCTGGTGGT

271 56

40 ProAlaArgPheIleValValProAlaAlaTyrAlaLeuAlaLeuGlyLe

alignment_scores:

Quality:

Ratio:

177.50 1.659 45.532

Gaps: Percent Identity:

13 30.638

Sequence 1534 BP;

235 A;

526 C;

479

G; 293

7;

1 other;

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allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthmorespiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                         asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of
                                                             nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA33923 to AAA3392) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequence
                                                                                                                                                                                                                      the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                             useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, and analysic activities. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a new composition comprising an
                                                                                                                                                                                                                                                                                                                                                                                                            ischaemic conditions, pulmonary vasoconstriction, allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-205971/18
                                            in
                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 1330; 1343pp; English
                                            sequence listing.
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322

73 lyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAlaLeuVal

89

uGlyLeuProAlaAsnValAlaAlaLeuAlaMetPheIleArgSerGlyG
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73

GGGGCTGCCGGCCAATGGGCTGGCGCTGTGGGTGCTGGCCACGCAGGCAC

272

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seq_documentation_block:
ID AAZ32747 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416
                                                                            cellular signalling; protease; tethered ligand; N-terminal; proteolysis; thrombin; trypsin; cleavage; hexapeptide; agon antagonist; cellular response; physiological response; clot platelet; proliferation; differentiation; mediation;
                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                          816
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                                                                                                                                                                                        Human protease-activated receptor PAR4 cDNA
                                                                                                                                                                                                                          31-JAN-2000
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                Homo sapiens
                                                                                                                                                   Protease-activated receptor; PAR4; ZCHEMR2; G protein coupled;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 GACCTCCTGCTGGCCCTGGCGCTGCCCCGGGGATCGCCTACCACCTGCG
                                                               inflammatory process; vascular injury; chemotaxis; mitogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                     GCTGGCCTCCGCCG...TGGCCTTCTTCGTGCCCAGCAACCTGCTGCTGC
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                                                                                                                                                                                                                                                                                                                                                 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAZ32747
                                                 factor;
                                                                                                                                                                                                                          (first entry)
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                                               production;
                                                                                                                                                                                                                                                                                               CDNA;
                                                                                                                                                                                                                                                                                              4895
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                                                                                                agonist;
clotting
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                                                                                                  pathway;
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alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                              alignment_block:
                                                                                                                                                                                     cc (PARs) are a subfamily of G protein coupled receptors which are capable of mediating cellular signalling in response to proteases (e.g., classes). They are characterised by a tethered peptide ligand at the cc extracellular N-terminus that is generated by proteolysis. PAR4 is cativated by thrombin or trypsin cleavage at Ry47/Gly48, which generates a new N-terminus corresponding to the tethered ligand (a hexapeptide). Cc Agonists of PAR4 are useful for upregulating cellular or physiological cresponses whereas antagonists are used to downregulate these cc activities. The PAR4 protein is further useful for dissecting the effects of thrombin or other activating proteases in the clotting capathway from the effects of these proteases at the cellular level. Cc Agonists are specifically useful in promoting the proliferation and/or differentiation of platelets, in mediating inflammatory events, cresponses to vascular injury, chemotaxis or mitogenesis, and in cc producing growth factors. Antagonists are useful as research reagents or characterising sites of ligand-receptor interaction.
 Align seg 1/1
                           US-09-899-513-2 x AAZ32747
                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human protease-activated receptor PAR4 (also referred to as ZCHEMR2) cDNA which was identified from EST (expressed sequence tag) sequences with homology to the three known protease-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 76-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    platelets and in mediating inflammatory events
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protease activated receptor 4, useful for screening for (ant)agonists for promoting the proliferation and/or differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-633640/54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1998;
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                                                                                                                                                              Sequence 4895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9950415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Presnell SR,
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to: AAZ32747
                                                                                                                                                              B₽;
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227..1330
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/product= "
1333..4895
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176..226
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1..175
                                                                         177.50
1.659
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176..1333
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                                                                                                                                                              971 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC
   from:
                                                                                                                                                               1573 C;
                                                                         Length: 235
Gaps: 13
Percent Identity: 30.638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human protease-activated receptor PAR4"
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40 ProAlaArgPheIleValValProAlaAlaTyrAlaLeuAlaLeuGlyLe

56

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAZ50775
                                                                                                                                                                                                                                 documentation_block:
AAZ50775 standard;
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                                                                                                                                       Human protease activated receptor-4 DNA.
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                                                                           antisense molecule; PAR antibody;
metastatic tumour cell; placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 lyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAlaLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCGGCTGCCCTCCACCATGCTG.....CTGATGAACCTCGCGACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCCACTGGCAACCGGCCTTCACCTGCCTGGCGCTGTTGGGCTGTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gTrp.SerSerProArgSerSerAlaCysAlaAlaAlaAlaSerTyrAla 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProThr.....ThrCysProProMetArgAr 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACCAGG.....CTGGTGCCCGCCCTCTATGGGCTGGTCCTGGTGGT
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                                             sapiens
                                                                                                          PAR-4; protease activated receptor;
                                                                                                                                                                      (first entry)
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Location/Qualifiers 176..1333
                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                               ... TGGCCTTCTTCGTGCCCAGCAACCTGCTGCTGC
                                                                                                                                                                                                                                    4895
                                                                                                                                                                                                                                    ВP
                                                                           cytostatic; therapeutic; implantation; invasive c
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method to treat metastatic tumour cells using an antisense molecule comprising a polynucleotide complementary to an RNA sequence of a protease activated receptor (PAR) protein, or an antibody capable of binding to a PAR protein. The antisense molecules antibodies of PAR protein are also used to treat disorders associated with implantation of placenta. The present sequence is a human PAR-4 DNA used for producing antisense molecules for treating invasive cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating metastatic tumor cells useful for treating disorders in placenta implantation in a female comprises administration of an antisense molecule complementary to an RNA sequence of a proteas activated receptor protein -
127 gTrp.SerSerProArgSerSerAlaCysAlaAlaAlaAlaSerTyrAla
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                                                                                                                                                                                                                                                                                                                    401 CCCACCAGG.....CTGGTGCCCGCCCTCTATGGGCTGGTCCTGGTGGT
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P-PSDB; AAY45036.
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                                                                                                                                                                                                                           lyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAlaLeuVal
                                                                                                                                                                                                                                                                GGGGCTGCCGGCCAATGGGCTGGCCGCGTGGCCACGCAGGCAC
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                                        GACCTCCTGCTGGCCCTGGCGCTGCCCCCGCGGATCGCCTACCACCTGCG
                                                                                                                                                                                                                                                                                          uGlyLeuProAlaAsnValAlaAlaLeuAlaMetPheIleArgSerGlyG
                                                                                               TGGCCAGCGCTTCGGGGAGGCCGCCTGCCGCCTGGCCACGGCCG
                                                                                                              ...........GlyLeuAlaArgArgProProAlaThrArgProGlyPro
                                                                                                                                                                            AspGluPhePheThrLeuThrLeuGlnLeuTrpLeuThrTyrTyr.Leu.
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Ratio:
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1.659
45.532
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/product= "PAR-4"
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Percent Identity:
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13
30.638
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involving

and

CTGGATCGCTACCTGGCCCTGGTGCACCCGCTGCGGGCCCGCGCCCTGCG

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seq_documentation_block:
ID AAH43632 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; protease-activated receptor; PAR4; N-terminal; activat platelet aggregation; inhibition; tumour cell; proliferation;
                                        Peptides comprising an amino acid sequence are capable of stimulating protease-activated receptor 4 which are useful in diagnosis and therapy e.g. inhibiting tumor cell proliferation and stimulating platelet
                                                                                                      WPI; 2001-656678/75.
P-PSDB; AAB47623.
                                                                                                                                                                                                            09-FEB-2000; 2000US-0500646
                                                                                                                                                                                                                                          06-FEB-2001; 2001WO-US03807
                                                                                                                                                                                                                                                                                                   WO200158930-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PAR4 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2002
Disclosure; Page 51-58;
                                                                                                                                                   Baindur N,
                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                       16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAH43632
                                                                                                                                                 West RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
191.1348
/*tag= a
                                                                                                                                                                                                                                                                                                                                              /product= "PAR4"
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                                                                                                                                                                                                                                                                                                                               "CDS derived
84pp; English
                                                                                                                                                                                                                                                                                                                                from protein AAB47623"
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alignment_block:
US-09-899-513-2 x AAH43632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes human protease-activated receptor, PAR4. Pep derived from, or based on, the N-terminal of activated PAR4 (see AAB47624-77), are capable of stimulating PAR4. These peptides may used to activate PAR4 at lower concentrations than wild type PAR4. These peptides may be used to stimulate platelet aggregation, and inhibiting tumor cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 CCCACCAGG.....CTGGTGCCCGCCCTCTATGGGCTGGTCCTGGTGGT
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Low adenosine antiset
KW human; airway disorde
KW surfactant depletion,
immunosuppressive; ar
immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. CC The antisense oligonucleotides and (I) can be used to down-regulate the CC expression and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and CC activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and CC chemokines, endogenously produced specific and non-specific enzymes, CC binding proteins, adhesion molecules and their receptors, cytokine and CC chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system creeptors, defensins, growth factors, vascactive peptides and CC receptors, binding proteins and malignancy associated proteins. The CC cantisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy(ies) CC and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, pulmonary implementation, palargy distress syndrome CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Low adenosine (A) content antisense oligonucleotides which do trigger adenosine receptors during metabolism, useful e.g. for cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; alrway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analyses; hypotensive; cytostatio;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1416-1418; 1592pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6546
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                                                                                                                                                                                                                                                                             inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONS reduces side effects. The Activities adapted to proper the containing ONS break down with the
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                                                                                                                                                              release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
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respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000
                                          invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequence given in the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1331-1333; 1343pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA
                                                                                                               differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGCCTCCGCCG...TGGCCTTCTTCGTGCCCAGCAACCTGCTGCTGC 2742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO:185
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Sequence

6546 BP; 1603 A;

1692 C;

1500 G;

1750 T; 1 other;

AX ID

AAX87944 standard; cDNA; 1174

sequences

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alignment_scores:
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seq_documentation_block:
                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX87944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 gTrp.SerSerProArgSerSerAlaCysAlaAlaAlaAlaSerTyrAla
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                                                                               GCTGGCCTCCGCCG
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                                                                                                                                                                                               pSerThrAlaGlyGlnAlaArgGly....
                                                                                                                                                                                                                                  TGCCCCTGCTGGCCATGCTGCTGCTACGGGGCCACCCTGCACACGCTG
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alignment_scores:
Quality:
Ratio:
                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of an isolated polynucleotide encoding a novel human G protein coupled receptor termed GPR25 (see AAY31751). The polynucleotide can be obtained from a cDNA library derived from mRNA in cells of human spleen using expressed sequence tag analysis. Treatment of a subject in need of GPR25 comprises administering GPR25, or a polynucleotide encoding a polypeptide that effects production of GPR25 in vivo, while treatment of a subject in need of inhibiting activity or expression treatment of a subject in need of inhibiting activity or expression
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P-PSDB; AAY31751.
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98US-0034985.
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g X XXXX 22-NOV-1999

(first entry)

/product= "Human APJ receptor"

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alignment_block:
US-09-899-513-2 x AAX87944
seq_documentation_block:
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                                                                                                            APJ receptor; HIV-1 coreceptor; SIV; cellular infection; envelope protein; env; CD4 coexpression; drug developmen
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alignment_block:
US-09-899-513-2 x AAA10298
                                                                                                                                                                                                                                              alignment_scores:
Quality:
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                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         can be used to identify compounds that modulate interaction between HIV and an APJ receptor, which may be useful in the development of anti-HIV drugs. Contacting cells expressing APJ and CD4 with an APJ binding/blocking agent (e.g., the antibodies or peptides) may be useful to inhibit HIV infection of such cells, e.g., to treat subjects having an HIV-related disorder associated with APJ expression. Antibodies and peptide fragments can be included in medicines and administered to treat patients (especially foetuses) having, or at risk of developing, an HIV infection or related disorder. The antibodies can also be used detect cells expressing the APJ receptor, and are useful to diagnose susceptibility to HIV infection. For example, higher APJ levels in
                                                                                                                                                                                                                                                                                                                                                       neuropathogenesis associated with HIV infection. Transgenic animals which express human CD4 and APJ proteins may provide model systems for the study of HIV infection and for anti-HIV drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant eukaryotic cells coexpressing APJ and CD4 polypeptides, useful for identifying compounds that modulate interaction between an HIV virus and an APJ receptor e.g. to develop anti-HIV drugs \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 9; 67pp; English
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                                                184 TCTCCACTCCCCAGCATGGAGGAAGGTGGTGATTTTGACAACTACTATGG
                                                                                                                                                                                                                                                                                                                       Sequence
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           yAspLeuGlyValGlyGlyCysSerLeuTrpAspAspProAlaArgPheI 44
                                                                                  SerAsnLeuSerSerAlaThrSerArgSerGluMetAsnSerSerValGl
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCGTGGGCTTTGTGGTGCCCTTCACCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACTAAGGTGCAGTGCTACATGGACTACTCCATGGTGGCCACTGTGAGC
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                                                                                                                                           domesticus
                                                                                                                                                                                            bone defects; ss
                                                                                                                                                                                                                                                                                                                                                                                            (first
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/product= chondrocyte protein
                                                                              Location/Qualifiers
                             /*tag=
                                                             . 954
                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that encoding a protein which is selectively expressed in chondrocytes in lower proliferative or upper hypertrophic zones of long bone and embryonic vertebrae growth plates. The protein is involved in the transition of chondrocytes from proliferation to hypertrophy. The product can be used for identifying the occurrence of proliferation or hypertrophy or the transition of chondrocytes from proliferation to hypertrophy in a tissue sample. It can also be used for preventing chondrocytes from transitioning from proliferation to hypertrophy and for inhibiting arthritic progression of articular chondrocytes in a patient. It can also be used for inducing chondrocytes to transition from proliferation to hypertrophy and for treating non-union bone defects.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated chondrocyte protein - which is involved in the transition of chondrocytes from proliferation to hypertroph to develop products for diagnosis and therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 954 BP; 157 A; 330 C; 308 G; 159 T; 0 other;
                                                                                                                                                                                                                                                                                        142 yrAlaValProGlyProGlyArgLeuProAlaTrpPro......Gly
                                                                                                                                                                                                                                                                                                                                                                126 gArgTrpSerSerProArg...SerSerAlaCysAlaAlaAlaAlaSerT 142
                                    GGGCCGCCGACATGGAACACCTGGCGCGCCGCC....TGGCCGCCC
                                                                                                                               .....GlyTrpArgAlaT 173
                                                                                                                                                                                  AlaTyrGlyAlaProArgAlaLeuProAlaProSerPro......
                                                                                                                                                                                                                                                          CCGCTACCCCACGGCCGGGCAAATCCGCCGCCTGGCCGAGCTGCACGGCC
                                                                                                                                                                                                                                                                                                                                                                                                     ArgProProAlaThrArgProGlyProProThrThrCysProProMetAr 126
                                                                      rpProLeuProAlaTrpSerThrAlaGlyGlnAlaArgGlyTrpProPro 189
                                                                                                            GCCTGGCCGATGTGGTACGAGGAGAGCCTCGACGGGCGGCGGCTGGCGCCGCG 362
                                                                                                                                                                                                                                                                                                                                .....CCTGCGCCCCGCTGCAGCTCCGCCGCGTCGTCCGCCACGGCAC 212
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2.621
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Gaps: 7
Percent Identity: 34.109
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....ArgTrpProSerAr 195
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seq_documentation_block:
ID AAV19864 standard: |
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV19864
                                                The sequence is that encoding a protein which is selectively expressed in chondrocytes in lower proliferative or upper hypertrophic zones of long bone and embryonic vertebrae growth plates. The protein is involved in the transition of chondrocytes from proliferation to hypertrophy. The product can be used for identifying the occurrence of proliferation or hypertrophy in a tissue sample. It can also be used for preventing chondrocytes from transitioning from proliferation to hypertrophy and for inhibiting arthritic progression of articular chondrocytes to transition from proliferation to hypertrophy and for inhibiting arthritic progression of articular chondrocytes to transition from proliferation to hypertrophy and for inhibiting arthritic progression of articular chondrocytes to transition from proliferation to
                                                                                                                                                                                                                                                                                                                               New isolated chondrocyte protein - which is involved in the transition of chondrocytes from proliferation to hypertrophy, used to develop products for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chondrocyte; transition;; proliferation; hypertrophy; diagnosis;
therapy; long bone; lower proliferative; upper hypertrophic;
embryonic vertebrae growth plates; arthritis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus domesticus chondrocyte protein gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 TCCAAGCACCGCTGCCTGCAGAGCGGCGCGCCTTCC 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-union bone defects; ss.
Sequence 1347 BP;
                                                                                                                                                                                                                                                                                              Claim 19; Pages 64-65; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-110224/10.
P-PSDB; AAW52286.
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                                  hypertrophy and for treating non-union bone defects.
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/product= chondrocyte protein
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 266 A; 432 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
 392 G;
 257 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
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alignment_scores:

Quality: Ratio:

162.50 2.621 48.062

Percent Identity:

34.109

Length: Gaps:

Percent Similarity:

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US-09-899-513-2 x AAV19864
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ID AAV19863 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
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WPI;
                                                                                                                                                                                                                                                                 chondrocyte; transition;; proliferation; hypertrophy; diagnosis; therapy; long bone; lower proliferative; upper hypertrophic; embryonic vertebrae growth plates; arthritis; treatment; non-union bone defects; ss.
                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 AlaTyrGlyAlaProArgAlaLeuProAlaProSerPro......
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                       Reynolds PR;
                                                                         05-JUL-1996;
                                                                                                                                                   WO9801468-A1
                                                                                                                                                                                                                                         Gallus domesticus.
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                                               (UYRP ) UNIV
                                                                                                 30-JUN-1997;
                                                                                                                          15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 GGGCCGCCGCGACATGGAACACCTGGCGCGCGCCCC....TGGCCGCCC
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1998-110224/10
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                                                  ROCHESTER
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81..1430
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alignment_block:
US-09-899-513-2 x AAV19863
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                                                                                                                                                                                                                                                                                                                                                                       293 CCGCTACCCCACGGCCGGGCAAATCCGCCGCCTGGCCGAGCTGCACGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gArgTrpSerSerProArg...SerSerAlaCysAlaAlaAlaAlaSerT 142
gPro.....ProSerCysTrpCysSerArgProThr 205
                                            GCTTCCCCGCGCTCTTCGCCGCCGCCGCCGCCTGGCGCTGGCCAGCAGC
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Ratio:
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seq_documentation_block:
ID AAV19861 standard; DNA; 2233 BP.
XX
AC AAV19861;

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV19861

TCCAAGCACCGCTGCCTGCAGAGCGGCGCGGCCTTCC 573

537

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                                                                                                                       Align seg 1/1 to: AAV19861
                                                                                                                                                      US-09-899-513-2 x AAV19861
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                              126
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            gArgTrpSerSerProArg...SerSerAlaCysAlaAlaAlaAlaAerT 142
                                                                             ArgProProAlaThrArgProGlyProProThrThrCysProProMetAr 126
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seq_documentation_block:
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The sequence is that encoding a protein which is selectively expressed in chondrocytes in lower proliferative or upper hypertrophic zones of long bone and embryonic vertebrae growth plates. The protein is involved in the transition of chondrocytes from proliferation to hypertrophy. The product
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DB; AAW52285.
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Quality:
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Percent Similarity:
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US-09-899-513-2 x AAV19860
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                                                                              487 GCTTCCCCGCGCTCTTCGCCGCCCGCCGCCGCCTGGCGCTGGCCAGCAGC 536
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537 TCCAAGCACCGCTGCCTGCAGAGCGGCGCGCCTTCC 573
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gb_est2:BF206181
gb_est2:BE337467
gb_est2:BE32753
gb_est2:BF259117
gb_est2:B1195434
gb_ess:AG063353
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gb_est2:BF195670
gb_est1:A1264420
gb_est1:A1277080
gb_est2:BF1008091
gb_est2:BF108800
gb_est2:AW072531
gb_est1:AW072531
                                                                         gb_est1:AL505079
gb_est1:AL506046
gb_est1:AI878854
                                                                                                                                                                                                                                                                                                                                                                 gb_est2:BF316851
gb_gss:CNS03JV6
gb_est1:AW055918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss:CNSO4N10
gb_est2:B1666779
b_est2:BF312953
_est2:BE259788
gb_est1:AL551285
gb_est1:AL561962
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Query: US-09-899-513-2
Query length: 205
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gb_est2:BF256597
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gb_est1:AW138178
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Database length: -1841457050
Search time (sec): 1692.580000
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                                                                                                                                                             gb_gss:CNS033KV
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-QGAPOP=4.500
-GGAPOP=4.500
-FGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
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-NO_XLPXY -WAIT -THREADS=1
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                                                                            BF253871 HVSMEf0002F16f Hordeun
AV23655 AV623655 Chlamydomonas
B1959810 HVSMEn0021K19f Hordeun
AL226264 Tetraodon nigroviridis
AL505079 AL505079 Hordeum vulga
AL505079 AL505079 Hordeum vulga
AL506046 Hordeum vulga
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US-09-899-513-2 x AI935035/rev
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                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AI935035
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                 44 eValValProAlaAlaTyrAlaLeuAlaLeuGlyLeuGlyLeuProAlaA 61
                                                                                                                                                                                                              28
                                                                                                                                                                                   AspLeuGlyValGlyGlyCysSerLeuTrpAspAspProAlaArgPheIl
snValAlaAlaLeuAlaMetPheIleArgSerGlyGlyArgLeuGlyGln
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seq_documentation_block: LOCUS AI935035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (127/)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 442.
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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I BM480059 AGENCOURT_6465042

I BG810205 mgct003xe24f Magna
I AG085604 Pan troglodytes DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est2:BF195670
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                      Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/ILNL, ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 bp mRNA linear EST 03-NOV-2000 7086906.xl NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571762 3' similar to contains TAR1.tl TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                 R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Be Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington Univers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 490)
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ocation/Qualifiers
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TITLE

Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata;
Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AspProAlaArgPheIleValValProAlaAlaTyrAlaLeuAlaLeuGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGATGAGTTCTTCACGCTCACGCTGCAGCTGTGGCTCACCTACTACCT
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                                                                                                   AI264420 460 bp mRNA linear EST 28-JAN-1999 gk54f04.xl NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1872799 3' similar to SW:P2Y4_HUMAN P51582 URIDINE NUCLECTIDE RECEPTOR ;, mRNA
                                    EST
                                                                      sequence.
AI264420
Homo sapiens
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Gaps: 0
Percent Identity: 98.734
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AUTHORS
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Quality:
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                                  hrCysProProMetArgArgTrpSerSerProArgSerSerAlaCysAla 137
                                                                                                                                           rLeuGlyLeuAlaArgArgProProAlaThrArgProGlyProProThrT 121
                                                                                                                                                                                                                            LeuValAspGluPhePheThrLeuThrLeuGlnLeuTrpLeuThrTyrTy 104
                                                                                                                                                                                                                                                                                                           erGlyGlyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAla 87
                                                                                                                                                                                                                                                                                                                                                                                           uGlyLeuGlyLeuProAlaAsnValAlaAlaLeuAlaMetPheIleArgS
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                                                                                                                                                                                                                                                                                        GCGGCGGGCCTGGCCAGGCCCTGCTTCTACCTGTTCAACCTGGCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspAspProAlaArgPheIleValValProAlaAlaTyrAlaLeuAlaLe
                                                                                                                     CCTGGGCCTGGCCGGAGGCCGCCTGCCACGCGGGGCCACCTACTA 211
                                                                                                                                                                                                       CTGGTTGATGAGTTCTTCACGCTCACGCTGCAGCTGTGGCTCACCTACTA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
a 151 c 179 g 42 t 1 others
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modified polylinker; 1st strand cDNA was prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         816.00
5.368
99.346
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/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:1872799"
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REFERENCE
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LOCUS AT277080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GCTGCGGCTTCGTACGCGGTCCCGGGCCCAGGGCGGCTGCCCGCCTGGCC
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                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 978 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mall.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 466) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                        /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:1874835"
/clone_lib="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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    Percent
  Identity:
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alignment_block: US-09-899-513-2 x AI277080/rev

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                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael
          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 449)
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Eukaryota; Metazoa;
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Gibco
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DEFINITION

BF108800 392 bp mRNA 17152h02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo

linear > sapiens

> EST 20-OCT-2000 CDNA clone

seq_documentation_block:

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US-09-899-513-2 x BF000091/rev
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                                                         erProGlyTrpArgAlaTrpProLeuProAlaTrpSerThrAlaGly
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                                      CGCCTGGCTGGCCCTGGCCTGCCTGGAGCACCGCTGGG
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gb_est2:BF108800
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Ratio:
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Location/Qualifiers
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99.329
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co16"
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REFERENCE
AUTHORS
TITLE
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US-09-899-513-2 x BF108800/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 715.00
Ratio: 5.500
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
126 gArgTrpSerSerProArgSerSerAlaCysAlaAlaAlaAlaSerTyrA 143
                                                                                                                                                                                                                                                                                             291 TCACGCTCACGCTGCACCTGTGCCTACTACCTGGGCCTGGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 yGlnAlaLeuLeuLeuTyrLeuPheAsnLeuAlaLeuValAspGluPheP 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AlaAsnValAlaAlaLeuAlaMetPheIleArgSerGlyGlyArgLeuGl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAACGTGGCGGCCCTGGCAATGTTCATCCGCAGCGGCGGGGGGCGCATGGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGCCCTGCTTCTACCTGTTCAACCTGGCTCTGGTTGATGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                       heThrLeuThrLeuGlnLeuTrpLeuThrTyrTyrLeuGlyLeuAlaArg 109
                                                                                                                                                                                              ArgProProAlaThrArgProGlyProProThrThrCysProProMetAr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF108800.1 GI:10938490 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE: 3525338 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbbHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbbHB-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from pools of 5,000 clones made from PCR-amplified cDNAs from PCR-amplified cDNAs
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a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3525338"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
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/db_xref="taxon:9606"
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REFERENCE
AUTHORS
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ORGANISM
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                          alignment_block:
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US-09-899-513-2 x AW072531/rev
                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 oAlaTrpSerThrAlaGlyGlnAlaArgGlyTrpProPro 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 ProArgAlaLeuProAlaProSerProGlyTrpArgAlaTrpProLeuPr 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laValProGlyProGlyArgLeuProAlaTrpProGlyAlaTyrGlyAla 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCGCGCGCTGCCTGCCCTTCGCCTGGCCGGCCCTGGCCCCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCTGGAGCACCGCTGGGCAAGCTCGGGGCTGGCCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL;

IMAGE Consortium (info@image.llnl.gov) for further !

Possible reversed clone: polyT not found

Insert Length: 872 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW072531 432 bp mRNA linear EST 20-Ox xa08e08.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567750 3' similar to contains PTR5.b2 TAR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  element ;, mRNA sequence. AW072531
                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 432. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 872 Std Erro
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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1 (bases 1 to 432)
                                                                                              Ratio:
                                                                                                                                                                                                                                                       84 a
                                                                                                                                                                                                                                               /note="Organ: pooled; vector: pT773D-Pac (Pharmacia) with /note="Organ: pooled; vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_GAP_GGB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                         . 689.50
4.856
97.260
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_NFL_T_GBC_S1"
                                                                         Percent Identity: 95.890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheThrLeuThrLeuGlnLeuTrpLeuThrTyrTyrLeuGlyLeuAlaAr 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAGGCCCTGCTTCTACCTGTTCAACCTGGCTCTGGTTGATGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est1:AW014139
                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Digo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWU14139 333 bp mRNA linear 1
UI-H-BIO-aaj-b-07-0-UI.sl NCI_CGAP_Subl Homo sapiens
IMAGE:2709445 3', mRNA sequence.
                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 236-273, >GC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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AW014139.1 GI:5862896
                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                        POLYA-No
                                                                                                                                        primer: M13 Forward
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2709445"
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                                                                                                 Location/Qualifiers
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US-09-899-513-2 x AW014139/rev
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332 CTGGCTATGGTTGATGAGTTATTCATGCTAACGCTGCAGCTGTGGCTCAC
169 lyTrpArgAlaTrpProLeuProAlaTrpSerThrAlaGlyGlnAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACTACCTGGGCCTGGCCCGGGGGCCGCCTCC.ACGCGGCCGGGGCCAC
                                                                                                                                                                                                                                                                                                                         TGTGCCGCTGCGGCTTCGTACGCGGTCCCGGGCCCAGGGCGGCTGCCCGC
                                                                                                                                       driver whose composition is detailed below: NCI_CGAP_Kid3

pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE
CloneIDs 1322376-1323911, 1456008 1456775, 1500552-1502855
) NCI_CGAP_Kid5 pool 1 LLAM 3388-3342, 3722-3725,
) NCI_CGAP_Kid5 pool 1 LLAM 3388-3342, 3722-3725,
) NCI_CGAP_Lid5 pool 1 LLAM 3388-3342, 3722-3725,
) NCI_CGAP_Lid5 pool 1 LLAM 3163-3725,
1471368-1477903, 1492104-1493255) NCI_CGAP_Lid5 pool 1 LLAM
3575-3582, 3851-3854 (IMAGE CloneIDs 1257096-1258631,
1520904-1522439) NCI_CGAP_CC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
1469064-1470983, 1475592-1476743) NCI_CGAP_Lid6 pool 1
14AM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
985608-986759, 1101192-1101959, 1217998-1220615)
NCI_CGAP_Col0 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs
1057446-1061255, 1144584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
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/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The
NCI_CGAP_Sub1 library is a subtracted library derived from
BI. BI constitutes a mixture of 21 normalized or
subtracted NCI_CGAP libraries: NCI_CGAP_Co10, NCI_CGAP_Co16
NCI_CGAP_PT22, NCI_CGAP_PT28, NCI_CGAP_Co10, NCI_CGAP_Co16
NCI_CGAP_RXid5, NCI_CGAP_RXid2, NCI_CGAP_Kid3,
NCI_CGAP_Kid11, NCI_CGAP_Kid12, NCI_CGAP_BT2, NCI_CGAP_Co8,
NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_BT2, NCI_CGAP_Lu5
, NCI_CGAP_Lu24, NCI_CGAP_Lei2, NCI_CGAP_GC4, NCI_CGAP_GC6
, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6
, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC6, NCI_CGAP_Lu19
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115 c 1
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TAG_LIB-NCI_CGAP_Br2
TAG_TISSUE-breast
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95.495
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Gaps: 0
Percent Identity: 92.793
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SE COUNT
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US-09-899-513-2 x BF307868
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Percent Similarity:
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TITLE
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                                                                                                                                           147
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                                                                                       rArgSerGluMetAsnSerSer.ValGlyAspLeuGlyValGlyGlyCys
 GGCAAGCGCTGGGGCACCTCTGGGAGGACCTTCACCAAGGTCAGAC
                                                                                                                                                                     {\tt GlyAlaAlaPheValAlaSerLeuArgSerAsnLeuSerSerAlaThrSe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601890683F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131836 5', mRNA_sequence.
                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1083)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                             <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e: LLCM1030 row: e column: 21 quality sequence stop: 466. Location/Qualifiers
                                                                     ATGAACAGCAGTGCTCGGGGACCTGGGTGTTGGCGGCTGC
                                                                                                                                                                                                             BF307868
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="rhabdomyosarcoma"
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 363 c 318 g 184 t
                                                                                                                                                                                                                                                                                             423.50
2.786
69.091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4131836"
/clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Identity:
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                                                                                                                                                                                                                                                                                                57.273
                                   51
                                                                     237
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                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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SOURCE
                                                                     FEATURES
                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AW014455
                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Mammalia; Eutheria;
1 (bases 1 to 220)
                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                             Tumor Gene Index
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                                                                                                   Seq primer: M13
                                                                                       POLYA=No.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2709396"
                                                                   Location/Qualifiers
                                                                                                       Forward
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175 LeuProAlaTrpSerThrAlaGlyGlnAlaArgGlyTrpProProProAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 gAla.....LeuProAlaProSerProGlyTrp...ArgAla.TrpPro 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 CTTGTGCACTTGGGCCTGTGGGCTGCCAGTCAATCGTGGCGGCCTGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ro.GlyProGlyArgLeuProAlaTrpProGlyAlaTyrGlyAlaProAr 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thr.ArgProGlyProProThrThrCysProProMetArgArg..TrpSe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rLeuPheAsnLeu.....AlaLeuValAspGluPhePheThrLeuThrL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetPheIleArgSerGly...GlyArgLeuGlyGlnAlaLeuLeuTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gTrp.....ProSerArgProProSerCys 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCCTCTGCAAGCACCTGCTGCGCCACCGCT.....CCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGCTAGACTAGCGCACTAAGCCCCTGGGCTGGCTCAGTGCCTTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGGACCAGGGCCGGCTCCCGCCTGGCCCGGTGCTACAGGCGCACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCGCCGCGCTCATCACGCGTGTGCCGCTGCCGGCTTCGTACAGCGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rSerProArgSerSer.AlaCysAlaAlaAla.AlaSerTyr.AlaValP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euGlnLeuTrpLeuThrTyrTyrLeuGlyLeuAlaArgArgProProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACTTCGGCCAGTGGAGAGCCTTCGATGGCTGCCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTTCATCCTGACGCGGCTGGCCGCCCTGGCCCAGGCCCTGCTTCTCTA
                   Email: cgapbs-r@mail.nih.gov Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW014455
UI-H-BIO-aai-a-07-0-UI.sl NCI_CGAP_Subl Homo sapiens IMAGE:2709396 3', mRNA sequence.
                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                            National Cancer Institute, Cancer
                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                            Genome
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                                                                                                                                                                                                                                                                                                                             Hominidae;
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                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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alignment_scores:
                                                                                                                                                                                                                                                             US-09-899-513-2 x AW014455/rev
                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                          169 TTCGTACGCGGTCCCGGGCCCAGGGCGGATGCCCGCCTGGCCCGGTGCAA 120
                                                                                                                                                                                                   124 ProMetArgArgTrpSerSerProArgSerSerAlaCysAlaAlaAlaAl
                                                                                                                                                                140 aSerTyrAlaValProGlyProGlyArgLeuProAlaTrpProGlyAlaT 157
                                                                                                                157 yrGlyAlaProArgAlaLeuProAlaProSerProGlyTrpArgAlaTrp 173
                                                                                                                                                                                       219 CCTATGCGGCGGTGGTCTTCGCCGCGCTAATCAGCGTGTGCCGCTGCGGC
                                          oArgTrpProSerArgPro 196
ACGGTGGCCGTCGCGGCCG 1
                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                           Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                           subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described [Bonaldo Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Two Approaches To Facilitate Gene Discovery.
                                                                                                                                                                                                                                                                                                                                                                                                    TAG_LIB=NCI_CGAP_Le12
TAG_TISSUE=le1omyosarcoma
                                                                                                                                                                                                                                                                                               351.00
5.400
89.041
                                                                                                                                                                                                                                                                                         Length: 73
Gaps: 0
Percent Identity: 86.301
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BASE COUNT ORIGIN

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JOURNAL COMMENT
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LOCUS AW138178
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TITLE
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ARA138178
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Oligo-GT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Seq primer: M13 Forward
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW138178.1 GI:6142578
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   28
                                                                                                                                                                                                 NCI_CGAP_Col6, NCI_CGAP_Kid1, NCI_CGAP_Lid2,
NCI_CGAP_Br2, NCI_CGAP_Col8, NCI_CGAP_CLL1, NCI_CGAP_Lid2,
NCI_CGAP_Br2, NCI_CGAP_Lid3, NCI_CGAP_Lid4,
NCI_CGAP_Br2, NCI_CGAP_Lid5, NCI_CGAP_Lid4,
NCI_CGAP_Brd2, NCI_CGAP_Lid5, NCI_CGAP_Lid4,
NCI_CGAP_Brd2, NCI_CGAP_Lid5, NCI_CGAP_Lid4,
NCI_CGAP_Brd2, NCI_CGAP_Lid5, NCI_CGAP_Lid4,
NCI_CGAP_Brd2, NCI_CGAP_Lid6,
NCI_CGAP_Lid1, NCI_CGAP_Col6,
NCI_CGAP_Lid1, NCI_CGAP_Col6,
NCI_CGAP_Lid1, NCI_CGAP_Col6,
NCI_CGAP_Kid3, pool 1
LLAM 3334-3337, 3682-3683,
13798-3803 (IMAGE CloneIDS 1323376-1323911, 1456008-1456775,
1500552-1502855); NCI_CGAP_Kid5 pool 1
LLAM 3372-3725, 376-3778 (IMAGE CloneIDS 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI_CGAP_Lid5 pool 1
LLAM 3375-3582, 3851-3854 (IMAGE CloneIDS 123912-1325831,
1471369-1522499); NCI_CGAP_COL9 pool 1
LLAM 3457-2459, 3751-3775 (IMAGE CloneIDS 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_Lid5 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 1257096-1258631,
14A8 4457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 1101192-1101959, 1217928-1220615);
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 1101192-1101959, 1217928-1220615);
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
LLAM 2457-2459, 2759-3062-3068 (IMAGE CloneIDS 1257096-1258631,
NCI_CGAP_COL0 pool 1
NCI_CGAP_COL0 
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                                                                                                        TAG_LIB=NCI_CGAP_GC4
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26
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gb_est1:AW138178

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REFERENCE
AUTHORS
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AUTHORS
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BASE COUNT
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Tetraodon nigroviridis genome survey sequence T7 end of clone
121H07 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetracdon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                           Unpublished 3 (bases 1
                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1026)
Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                 121
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               /clone_lib="G"
/note="Genoscope
367 c 348
                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="121H07"
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                                                                            LOCUS BI666779
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                                                                                                                        gb_est2:BI666779
BI666779.1 GI:15581012
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                                                            603291708F1 NIH_MGC_96
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                                              euAlaArgArgProProAlaThrArgProGlyProProThrThrCysPro 123
                                                                                                                                                    pGluPhePheThrLeuThrLeuGlnLeuTrpLeuThrTyrTyrLeuGlyL 107
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11788 row: o column:
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1 (bases 1 to 758)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

191 c 311 g 83 t
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/clone_11b="NIH_MGC_96"
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/lab_host="DH10B"
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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alignment_scores:

Gene Collection (MGC)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....SerLeuTrpAspAspProAlaArgPheIleV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....GCCTCCAGCCTCGTCGCAGCTGCGGCCCAGGGCCCCTGAAGC 209
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                                                                                                                                                                                                                   601152574F1 NIH_MGC_19 Homo sapiens
                             Homo sapiens
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                                                                                                                           BE259788.1 GI:9130544
                                                                                                                                                                                      mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                            .CCTCCCACTCCTTGGAGAGCCGCTCCTCCT
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                       139 laAlaSer.....TyrAlaValProGlyProGlyArgLeuProAla
                                                                                                                                                        323
                                                                                                                                                                                                                122 sProProMetArgArgTrpSerSerProArgSerSerAlaCysAlaAlaA 139
                                                                                                                                                                                                                                                                                    367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 CCTGCCAGCCGGTGTCTCAGCCCCGCCGTAGTGCCTGCAGCTGGGGGGCC 518
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                                                                                                                                                                                                                                                                                                                                           106 GlyLeuAlaArgArgProProAlaThrArgProGlyProProThrThrCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GlyArgLeuGlyGlnAlaLeuLeuLeuTyrLeuPheAsn.LeuAlaLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 uGlyLeuProAlaAsnValAlaAlaLeuAlaMetPheIleArgSerGly. 72
                                                                                                                                                                                                                                                                                                                                                                                                         alAspGluPhePheThrLeuThrLeuGlnLeuTrpLeuThrTyrTyrLeu 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCACATTTCTCCAGCTCTGCCTCAATGGCCGACAGGCTCTCCAGCTCC
                                CGGCCCAGGGCCCCTGAAGCCGTAGGCCCCGGGCCCCGGAAGGAGCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 571.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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/clone_Lib="NIH_MGC_19"
/clone_Lib="NUH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)
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/db_xref="taxon:9606"
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